

Sequence	Strid	Orig	ZScore	EScore	Len	Documentation
gb_pat:AX005896	+	81.00	303.58	1.2e-08	51	AX005896 Sequence 105 from Paten
gb_pat:AX005857	+	81.00	284.25	1.5e-07	453	AX005857 Sequence 66 from Paten
gb_pl:TAE242531	+	81.00	271.50	4.7e-07	1872	AJ242531 Triticum aestivum th
gb_pat:AX005805	+	81.00	270.78	7.8e-07	2125	AX005805 Sequence 14 from Paten
gb_pat:AX005794	+	81.00	268.43	1.1e-06	2709	AX005794 Sequence 3 from Paten
gb_pat:AX005807	+	78.00	276.71	3.9e-07	302	AX005807 Sequence 16 from Paten
gb_pat:AX005808	+	78.00	274.89	4.9e-07	371	AX005808 Sequence 17 from Paten
gb_pat:AX005803	+	78.00	268.43	1.1e-06	770	AX005803 Sequence 12 from Paten
gb_pl:ZMA242530	+	78.00	260.48	3.1e-06	1890	AJ242530 Zea mays partial d g
gb_pat:AX005806	+	78.00	258.92	3.8e-06	2255	AX005806 Sequence 15 from Paten
gb_pl:AB030956	+	78.00	258.01	4.3e-06	2500	AB030956 Oryza sativa mrna for
gb_pl:AC087797	+	78.00	223.58	0.0004	122497	AC087797 Oryza sativa chromo
gb_pat:AX005810	+	72.00	246.70	1.8e-05	725	AX005810 Sequence 19 from Paten
gb_pat:AX005867	+	70.00	246.40	1.9e-05	324	AX005867 Sequence 76 from Paten
gb_pl:ATRG42	+	70.00	230.52	0.0001	1951	Y11337 A.thaliana mrna for RGA
gb_pat:AG4697	+	70.00	230.46	0.0001	1964	AG4697 Sequence 1 from Paten
gb_pl:ATV15193	+	70.00	230.46	0.0001	1964	Y15193 Arabidopsis thaliana GR
gb_pl:ATV15194	+	70.00	229.45	0.0002	2201	Y15194 Arabidopsis thaliana GR
gb_pl:ATRG41	+	70.00	229.42	0.0002	2210	Y11336 A.thaliana mrna for RGA
gb_pl:ATX242957	+	70.00	223.99	0.0003	4081	AJ242957 Arabidopsis thaliana
gb_pl:ATFKM16	+	70.00	207.40	0.0028	26604	AL391150 Arabidopsis thaliana
gb_pl:ATAC009895	+	70.00	197.41	0.0102	82289	AC009895 Arabidopsis thaliana
gb_pl:ATAC020665	+	70.00	197.05	0.0106	85702	AC020665 Arabidopsis thaliana
gb_pl:AC005560	-	70.00	196.13	0.0120	95137	AC005560 Arabidopsis thaliana
gb_pl:AC006917	-	70.00	193.18	0.0175	132699	AC006917 Genomic sequence fo
gb_pat:AX081276	+	66.00	216.49	0.0009	1779	AX081276 Sequence 1 from Paten
gb_pat:AX081278	+	66.00	216.49	0.0009	1779	AX081278 Sequence 3 from Paten
gb_pat:AX005860	+	65.00	232.12	0.0001	200	AX005860 Sequence 69 from Paten
gb_pat:AX005809	+	62.00	214.51	0.0011	416	AX005809 Sequence 18 from Paten
gb_pl:AF224770	+	51.00	171.65	0.2765	524	AF224770 Andira aubletii clone
gb_htg:AC015886	-	49.00	112.15	570.13	188716	AC015886 Mus musculus clone
gb_pr:AL355796	-	48.00	110.35	718.29	125086	AL355796 Human DNA sequence
gb_pl:AC007504	-	47.00	108.37	925.55	125021	AC007504 Arabidopsis thalian
gb_htg:AC034100	-	47.00	105.17	1.4e+03	179481	AC034100 Mus musculus chromo
gb_da:AP002997	-	47.00	99.79	2.8e+03	329709	AP002997 Mesorhizobium ltr
gb_pat:AX005855	+	46.00	157.77	1.64	309	AX005855 Sequence 64 from Paten
gb_da:RPXX02	+	46.00	96.56	4.2e+03	312430	AJ235271 Rickettsia prowazek
gb_pl:HBU40402	+	45.00	143.01	10.89	1078	U40402 Hevea brasiliensis hydr
gb_pat:A59586	+	45.00	142.90	11.04	1091	A59586 Sequence 1 from Paten
gb_htg:AC026377	-	45.00	98.68	3.2e+03	161592	AC026377 Mus musculus chromo

gb_ba:AE001520	10516	1	AE001520 Helicobacter pylori,	gb_ba:AF064682	3664	1	AF064682 Porphyromonas ging
gb_pat:AX191747	602.21	-	AX191747 Sequence 29 from Pat	gb_v1:CFU19239	4000	-	U19239 Chorisiconura fumifera
gb_ba:AE000606	615.42	-	AE000606 Helicobacter pylori	gb_to:MMU21795	5267	-	U21795 Mus musculus common
gb_pl:EU003904	783.05	-	U03904 Emericichia nidulans cy	gb_pl:AF053008	8301	-	AF053008 Glycine max env ps
gb_ba:AY005136	843.73	-	AY005136 Chlorobium tepidum F	gb_ba:AE007865	8712	-	AE007865 Clostridium acetob
gb_pl:ATU53501	100.46	+	U53501 Arabidopsis thaliana C	gb_ba:AE002398	10629	+	AE002398 Nelisseria meningi
gb_in:AC0017345	98.89	+	AC017345 Drosophila melanog	gb_ba:AE004239	10704	+	AE004239 Vibrio cholerae c
gb_in:AC004115	93.76	+	AC004115 Drosophila melanog	gb_ba:AE005186	12518	+	AE005186 Escherichia coli
gb_pl:F23A5	90.98	+	AC003040 Arabidopsis thaliana	gb_vt:LDVGLVPOL	13699	+	AL10529 Homo sapiens chro
gb_pr:AL158152	90.60	+	AL158152 Human DNA sequence	gb_ba:AE002550	15053	+	AE002550 Nelisseria meningi
gb_pr:AF000997	89.44	+	AF000997 Homo sapiens DNA, C	gb_ba:AE000736	15862	+	AE000736 Aquifex aeolicus
gb_pr:AC078864	88.89	+	AC078864 Homo sapiens chromo	gb_ba:AE004132	16251	+	AE004132 Vibrio cholerae c
gb_pr:AC007314	88.46	+	AC007314 Homo sapiens BAC cl	gb_ba:AE000118	21757	+	AE000118 Escherichia coli
gb_htg:AC019244	88.46	+	AC019244 Homo sapiens clone	gb_ba:EC2MIN	28277	+	X5034 E. coli 2 minute re
gb_htg:AC007924	87.66	+	AC007924 Homo sapiens chromo	gb_pat:AX191720	28277	+	AX191720 Sequence 2 from P
gb_htg:AL445653	87.59	+	AL445653 Homo sapiens chromo	gb_pr:AC002306	38651	+	AC02306 Homo sapiens DNA
gb_in:AC008371	87.45	+	AC008371 Drosophila melanog	gb_pr:SPAC13D3	39292	+	L68166 S.pombe chromosome
gb_htg:AF003372	87.40	+	AF003372 Oryza sativa chromo	gb_htg:AC035148	39292	+	Continuation (4 of 4) of A
gb_pr:CN501450	87.38	+	AL135858 Human chromosome 14	gb_htg:AC0393D12	58383	+	Continuation (4 of 4) of A
gb_htg:AC084819	87.34	+	AC084819 Homo sapiens chromo	gb_htg:HSJ393D12	58383	+	Continuation (4 of 4) of A
gb_htg:AC087784	87.24	+	AC087784 Homo sapiens chromo	gb_pr:SCU12980	97137	+	U004745 Homo sapiens BAC
gb_htg:AF002991	87.21	+	AF002991 Homo sapiens chromo	gb_pl:SCU12980	103682	+	U12980 Saccharomyces cere
gb_htg:AL356126	87.07	+	AL356126 Homo sapiens chromo	gb_htg:AC011458	105412	+	AC011458 Homo sapiens chr
gb_htg:AC027624	86.99	+	AC027624 Homo sapiens chromo	gb_htg:AC035148	107850	+	AC035148 Homo sapiens chr
gb_htg:AL512424	86.97	+	AL512424 Homo sapiens chromo	DI0483	111401	+	DI0483 E.coli K12 genome,
gb_htg:AC087241	86.89	+	AC087241 Homo sapiens chromo	gb_htg:AC010107	112958	+	AC010107 Drosophila melan
gb_htg:AC025622	86.82	+	AC025622 Mus musculus clone	AC027441	116230	+	AC027441 Homo sapiens chr
gb_htg:AC025349	86.82	+	AC025349 Homo sapiens chromo	AC027441	116230	+	AC027441 Homo sapiens chr
gb_htg:AF003902	86.75	+	AF003902 Oryza sativa chromo	AC000887	120684	+	AC000887 Homo sapiens gen
gb_htg:AC026286	86.50	+	AC026286 Homo sapiens chromo	AC079626	122728	+	AC079626 Mus musculus chr
gb_htg:AC034251	86.40	+	AC034251 Homo sapiens chromo	AL139090	128468	+	AL139090 Human DNA sequen
gb_htg:AC034511	86.25	+	AC034511 Homo sapiens chromo	AL034343	130904	+	AL034343 Human DNA sequen
gb_htg:AL591376	85.57	+	AL591376 Mus musculus clone	AL359096	131299	+	AL359096 Homo sapiens chr
gb_htg:AC079529	85.26	+	AC079529 Mus musculus clone	AC022926	136883	+	AC022926 Homo sapiens chr
gb_htg:AC028259	85.12	+	AC028259 Homo sapiens 12 BAC	AP000405	141675	+	AP000405 Homo sapiens chr
gb_htg:AC079426	85.02	+	AC079426 Mus musculus chromo	AP001038	141859	+	AP001038 Homo sapiens gen
gb_htg:AC073717	85.02	+	AC073717 Mus musculus clone	AC028442	142592	+	AC028442 Homo sapiens chr
gb_htg:AC093339	84.93	+	AC093339 Mus musculus clone	AC073826	146190	+	AC073826 Mus musculus clo
gb_htg:AL513345	84.26	+	AL513345 Mus musculus chromo	AC009943	150236	+	AC009943 Homo sapiens clo
gb_in:AE003732	84.26	+	AE003732 Drosophila melanog	AL450103	153914	+	AL450103 Homo sapiens chr
gb_htg:AL596136	83.37	+	AL596136 Mus musculus chromo	AC073295	154256	+	AC073295 Mus musculus clo
gb_htg:AL359385	83.37	+	AL359385 Homo sapiens chromo	AL359714	156129	+	AL359714 Human DNA sequen
gb_in:AE003589	82.00	+	AE003589 Drosophila melanog	AP002542	156266	+	AP002542 Oryza sativa gen
gb_ba:TACID1	80.86	+	AL45063 Thermoplasma acidop	AC022795	157888	+	AC022795 Homo sapiens chr
gb_pat:116698	141.64	+	116698 Sequence 43 from patent	AC080158	160203	+	AC080158 Mus musculus chr
gb_pat:AX005865	139.94	+	AX005865 Sequence 74 from Patent	AP000888	166355	+	AP000888 Homo sapiens gen
gb_htg:AC089106	135.19	+	AC089106 Giardia intestinalis c	AC061122	166953	+	AC061122 Homo sapiens chr
gb_to:S75844S8	135.55	+	S75852 IL-2R gamma -interleukin	AC021774	167366	+	AC021774 Homo sapiens clo
gb_ba:D78201	131.79	+	D78201 Borrelia miyamotoi gene	AC084290	168249	+	AC084290 Homo sapiens chr
gb_ba:AB001719	131.77	+	AB001719 Borrelia miyamotoi str	gb_htg:AL356260	168464	+	AL356260 Homo sapiens chr
gb_sts:CN506KJX	129.03	+	AB02979 T7 end of clone AT0AAG	gb_htg:AC035322	169670	+	AL356260 Homo sapiens chr
gb_ba:S81109	126.50	+	S81109 citrate synthase [Pyroc	gb_htg:AC024662	170558	+	AL596444 Mus musculus chr
gb_ba:AF015823	125.83	+	AF015823 Streptomyces venezuel	gb_pr:AC015973	171549	+	AC024662 Homo sapiens chr
gb_pat:AX189061	125.39	+	AX189061 Sequence 262 from Pat	gb_htg:AC015973	171834	+	AC015973 Homo sapiens BAC
gb_to:MUS12RGA	124.73	+	D13565 Mus musculus mRNA for i	gb_pat:AX044035	173325	+	AX044035 Sequence 114 fro
gb_pat:AR072026	124.63	+	AR072026 Sequence 1 from patent	gb_htg:AC037348	175371	+	AC073748 Mus musculus clo
gb_to:MM12RGC	124.63	+	AR072026 Sequence 1 from patent	gb_htg:AC087868	178676	+	AC087868 Mus musculus clo
gb_to:ECMURGC	124.55	+	L20048 Mouse interleukin 2 rec	gb_htg:AC087868	179032	+	AC087868 Homo sapiens chr
gb_to:U95086	124.07	+	X75337 M.musculus mRNA for mur	gb_htg:AC022809	179376	+	AC022809 Homo sapiens chr
gb_to:U95086	123.63	+	X52540 Escherichia coli cell-e	gb_htg:AC007961	179637	+	AC007961 Mus musculus chr
gb_pat:AX166563	122.75	+	U95086 Mus musculus AtptA gene	gb_htg:AP001352	179637	+	AP001352 Homo sapiens chr
gb_pat:AX166563	122.75	+	U67892 Escherichia coli UDP-Mu	gb_htg:AL360090	181936	+	AL360090 Homo sapiens chr
gb_ba:ECU67892	122.75	+	X52644 Escherichia coli murG a	gb_htg:AC092215	183533	+	AC092215 Mus musculus clo
gb_ba:ECMURGC	122.75	+	X52644 Escherichia coli murG a	gb_htg:AC084402	184747	+	AC084402 Mus musculus chr
gb_pr:AC033118	119.74	+	AB033118 Homo sapiens mRNA for	AP000063	185300	+	AP000063 Aeropyrum pernix
gb_pl:YSCFN12A	118.89	+	L29389 Saccharomyces cerevisia	gb_htg:AC073561	185699	+	AC073561 Mus musculus chr

gb_htg:AL355513	174552	1	AL355513	Homo sapiens	chromid	103.50	1.7e+03	11513	AF353728	Mus musculus	myo-
gb_htg:AL591711	20875	1	AL591711	Mus musculus	chromid	102.51	2.0e+03	12879	AE004609	Pseudomonas	aerug
gb_pr:AL351833	201512	1	AL351833	Human DNA	sequence	101.70	2.2e+03	14104	U15146	Lactate dehydrogena	
gb_htg:AC084827	202052	1	AC084827	Mus musculus	clone	98.96	3.1e+03	19227	AR118085	Sequence 13	from
gb_htg:AC010413	203876	1	AC010413	Homo sapiens	chromid	98.59	3.2e+03	20062	AE003919	Xylella fastidiosa	
gb_htg:AC073749	206533	1	AC073749	Mus musculus	clone	97.83	3.6e+03	21852	298056	S.pombe	chromosome
gb_htg:AC079988	203378	1	AC079988	Homo sapiens	chromid	97.00	4.0e+03	24000	AE004856	Pseudomonas	aerug
gb_htg:AC073828	203378	1	AC073828	Mus musculus	clone	96.80	4.1e+03	24550	271259	Caenorhabditis	eleg
gb_htg:AC087153	216133	1	AC087153	Mus musculus	clone	96.73	4.1e+03	24753	AL031710	Human DNA	sequence
gb_htg:AC079272	227366	1	AC079272	Mus musculus	clone	95.61	4.8e+03	28080	AF016438	Caenorhabditis	el
gb_htg:AL591514	230933	1	AL591514	Mus musculus	chromid	95.02	5.1e+03	30037	U49940	Caenorhabditis	eleg
gb_htg:AL596103	232712	1	AL596103	Mus musculus	chromid	92.73	6.9e+03	38875	AC006950	Homo sapiens	chro
gb_ba:AP000003	233004	1	AP000003	Pyrococcus horikoshii		92.45	7.1e+03	40138	AR118084	Sequence 12	from
gb_htg:AC073760	237653	1	AC073760	Mus musculus	clone	92.14	7.4e+03	41567	AB025342	Moritella marina	
gb_htg:AC093263	241309	1	AC093263	Homo sapiens	chromid	91.63	7.9e+03	44042	AL023705	S.pombe	chromosome
gb_pr:AC097989	243675	1	AC097989	Mus musculus	9 BAC	87.72	1.3e+04	68484	AL355926	Neurospora crassa	
gb_htg:AC090887	248494	1	AC090887	Mus musculus	clone	86.24	1.6e+04	80993	AC004313	Drosophila	melano
gb_htg:AC073822	247196	1	AC073822	Mus musculus	clone	85.96	1.6e+04	83551	AC018150	Drosophila	melano
gb_ba:AP000250	281530	1	AP000250	Escherichia coli	O157:H7	85.70	1.7e+04	86043	AC084694	Mus musculus	***
gb_ba:CNBPAX05	304290	1	AJ248287	Pyrococcus abyssi	strain	85.15	1.8e+04	91570	AL080282	Arabidopsis	thali
gb_htg:AC093082	326924	1	AC093082	Homo sapiens	chromid	84.33	2.0e+04	100499	AL138769	Human DNA	sequence
gb_pr:AP001732	340000	1	AP001732	Homo sapiens	genomic	84.17	2.1e+04	102308	AC005231	Homo sapiens	PAC
gb_ba:AP003001	345783	1	AP003001	Mesorhizobium loti		83.53	2.2e+04	110000	Continuation (3 of 5) of		
gb_ba:AP001118	347550	1	AP001118	Buchnera sp.	APS 96	83.07	2.4e+04	115932	AL031589	Human DNA	sequence
gb_ba:NMA222491	349061	1	AL162753	Neisseria meningitidis		82.91	2.4e+04	117955	AC019052	Homo sapiens	cio
gb_pat:AX041921	349980	1	AX041921	Sequence 816	from H	82.84	2.4e+04	118929	AC025976	Homo sapiens	chr
gb_pat:AX044029	349980	1	AX044029	Sequence 108	from H	82.84	2.4e+04	118929	AC025976	Homo sapiens	chr
gb_pat:AX044034	349980	1	AX044034	Sequence 113	from H	82.73	2.5e+04	120423	AL023279	Homo sapiens	DNA
gb_in:AF189278	16611	1	AF189278	Drosophila melanogaster		82.44	2.6e+04	124937	AL022152	Homo sapiens	DNA
gb_ba:AE008219	9588	1	AE008219	Agrobacterium tumefaciens		82.19	2.7e+04	124937	AC073709	Mus musculus	cio
gb_htg:AC007995	204206	1	AC007995	Mus musculus	clone	81.77	2.8e+04	134222	AB045363	Homo sapiens	gen
gb_in:AE003516	287649	1	AE003516	Drosophila melanogaster		81.42	2.9e+04	136665	AP000865	Homo sapiens	chr
gb_pl:VNA401056	222	1	AJ401056	Vicia narbonensis	Ty1-	80.54	3.3e+04	154309	AL592437	Homo sapiens	chr
gb_pat:AX005861	230	1	AX005861	Sequence 70	from Pat	80.26	3.4e+04	159173	AC015992	Homo sapiens	chr
gb_sts:AU027871	251	1	AU027871	Rattus norvegicus	ONS	80.21	3.4e+04	160125	AC016947	Homo sapiens	chr
gb_sts:G23444	395	1	L00124	Rat elastase II gene	exon	80.15	3.4e+04	161175	AC073758	Mus musculus	cio
gb_sts:G23444	423	1	G23444	human STS SHGC-33656	seq	80.09	3.5e+04	162269	AC000097	Homo sapiens	chr
gb_htg:AC037213	453	1	G23444	human STS SHGC-33656	seq	80.02	3.5e+04	163579	AC018635	Homo sapiens	chr
gb_htg:AC037213	603	1	AC037213	Giardia intestinalis	clone	79.94	3.5e+04	165073	AC073516	Homo sapiens	chr
gb_pat:AX142463	603	1	AX142463	Sequence 1185	from Pat	79.93	3.5e+04	165243	AL162408	Homo sapiens	chr
gb_htg:AC028609	819	1	AC028609	Giardia intestinalis	clone	79.86	3.6e+04	166564	AC026101	Homo sapiens	chr
gb_htg:AC028609	918	1	AC028609	Giardia intestinalis	clone	79.85	3.6e+04	166751	AC087086	Rattus norvegicus	
gb_htg:AC037121	954	1	AC037121	Giardia intestinalis	clone	79.84	3.6e+04	166892	AC007463	Homo sapiens	BAC
gb_htg:AC037121	982	1	AC037121	Giardia intestinalis	clone	79.80	3.6e+04	167691	AL023284	Human DNA	sequence
gb_htg:AC037121	1043	1	AC037121	Giardia intestinalis	clone	79.73	3.6e+04	168990	AC064834	Homo sapiens	cio
gb_htg:AC037121	1059	1	AC037121	Giardia intestinalis	clone	79.63	3.7e+04	170983	AL590117	Homo sapiens	chr
gb_htg:AC037121	1086	1	AC037121	Giardia intestinalis	clone	79.57	3.7e+04	172114	AP001999	Homo sapiens	chr
gb_htg:AC037121	1090	1	AC037121	Giardia intestinalis	clone	79.54	3.7e+04	172797	AC001298	Homo sapiens	chr
gb_htg:AC037121	1101	1	AC037121	Giardia intestinalis	clone	79.43	3.8e+04	174840	AC006549	Homo sapiens	chr
gb_htg:AC037121	1109	1	AC037121	Giardia intestinalis	clone	79.38	3.8e+04	175925	AC068110	Homo sapiens	chr
gb_htg:AC037121	1424	1	BC003930	Mus musculus	RIKEN	79.23	3.9e+04	178944	AP000804	Homo sapiens	chr
gb_htg:AC037121	1550	1	AF306766	Pseudomonas aeruginosa		79.21	3.9e+04	179269	AC006547	Homo sapiens	chr
gb_htg:AC037121	1700	1	AF10740	Pseudomonas aeruginosa		79.14	3.9e+04	180742	AL359753	Human DNA	sequence
gb_htg:AC037121	2191	1	Y5415	IPilG-interferon-inducible		79.12	3.9e+04	181047	AC016765	Homo sapiens	chr
gb_htg:AC037121	2593	1	X12672	Bovine mRNA for oploid		79.08	3.9e+04	181902	AC020788	Homo sapiens	chr
gb_htg:AC037121	3035	1	AF270268	Arabidopsis thaliana		78.97	4.0e+04	184180	AL589623	Mus musculus	chr
gb_htg:AC037121	3246	1	AF270268	Staphylococcus epidermidis		78.96	4.0e+04	184433	AL596446	Mus musculus	chr
gb_htg:AC037121	3246	1	AX145606	Sequence 4328	from Pa	78.95	4.0e+04	184651	AL450317	Mus musculus	chr
gb_htg:AC037121	3645	1	AF269682	Staphylococcus epidermidis		78.93	4.0e+04	184929	AC058790	Homo sapiens	chr
gb_htg:AC037121	3645	1	AX145002	Sequence 3724	from Pa	78.85	4.1e+04	186729	AC01296	Pan troglodytes	
gb_htg:AC037121	4248	1	AF269845	Staphylococcus epidermidis		78.79	4.1e+04	188034	AC036169	Homo sapiens	chr
gb_htg:AC037121	4248	1	AX145163	Sequence 3885	from Pa	78.76	4.1e+04	188561	AL592488	Homo sapiens	chr
gb_htg:AC037121	5260	1	U05958	Squalus acanthias	bunnet	78.71	4.1e+04	189612	AC051617	Mus musculus	cio
gb_htg:AC037121	7374	1	AF201894	A-2 plaque virus A2	H	78.57	4.2e+04	192782	AC079276	Mus musculus	chr
gb_htg:AC037121	7894	1	AF060248	Arabidopsis thaliana		78.44	4.3e+04	195630	AC087898	Mus musculus	chr
gb_htg:AC037121	10529	1	AE005138	Halobacterium sp.	NH	78.42	4.3e+04	195931	AC068174	Homo sapiens	chr
gb_htg:AC037121	10640	1	AE006777	Sulfolobus solfataricus		78.39	4.3e+04	196606	AP000779	Homo sapiens	gen
gb_htg:AC037121	10651	1	AE007899	Agrobacterium tumefaciens		78.39	4.3e+04	196722	AC092481	Mus musculus	cio
gb_htg:AC037121	10694	1	AE004474	Pseudomonas aeruginosa		78.35	4.3e+04	197568	AL161553	Arabidopsis	thal
gb_htg:AC037121	10993	1	AE007244	Sinorhizobium meliloti		78.30	4.3e+04	198602	AL450395	Mouse	DNA
gb_htg:AC037121	11154	1	AE006890	Sulfolobus solfataricus		78.30	4.3e+04	198715	AL161554	Arabidopsis	thal
gb_htg:AC037121	11208	1	X57144	H. halobium RNA	polym	78.30	4.3e+04	198739	AC079840	Homo sapiens	chr

gb_hhg:AC074027	+	40.00	78.27	4.4e-04	199359	!	AC074027	Mus musculus chromo	gb_hhg:AC018135	-	39.00	108.58	901.38	4264	!	AC018135	Drosophila melanog
gb_hhg:AC034116	+	40.00	78.23	4.4e-04	200254	!	AC034116	Mus musculus clone	gb_ov:DFGAGR	-	39.00	108.39	923.00	4354	!	M45123	Discopyge ommata (Cl
gb_hhg:AL596386	+	40.00	78.21	4.4e-04	200720	!	AL596386	Mus musculus chromo	gb_ov:EGOPATBCD	-	39.00	108.33	930.46	4385	!	L64149	E.coli transport pro
gb_hhg:AC064868	-	40.00	78.20	4.4e-04	200859	!	AC064868	Homo sapiens chromo	gb_ba:AE077856	+	39.00	108.31	932.87	4395	!	AF077856	Actinobacillus act
gb_pr:AP001256	-	40.00	78.04	4.5e-04	204699	!	AP001256	Homo sapiens genom	gb_ba:AE077856	+	39.00	108.31	932.87	4395	!	E33370	NA+ATPase gene. 2/2
gb_hhg:AC073792	-	40.00	78.03	4.5e-04	204929	!	AC073792	Mus musculus clone	gb_pat:R33370	-	39.00	108.17	950.23	4467	!	E33370	NA+ATPase gene. 2/2
gb_hhg:AL591032	-	40.00	77.99	4.5e-04	205676	!	AL591032	Mus musculus chromo	gb_pr:AK023832	-	39.00	107.91	981.43	4596	!	AC023832	Homo sapiens cDNA
gb_hhg:AL591032	-	40.00	77.97	4.5e-04	206191	!	AL591032	Mus musculus chromo	gb_pr:CRUKCG1	-	39.00	107.79	997.48	4623	!	L72331	Cricetulus griseus (
gb_hhg:AC074161	-	40.00	77.79	4.6e-04	210539	!	AC074161	Mus musculus clone	gb_pl:ATU63931	+	39.00	107.69	997.48	4662	!	U63931	Arabidopsis thaliana
gb_hhg:AC025751	+	40.00	77.61	4.7e-04	214894	!	AC025751	Mus musculus clone	gb_pr:AC028950	+	39.00	107.71	1.0e+03	4704	!	AB028950	Homo sapiens mRNA
gb_hhg:AC073812	+	40.00	77.44	4.9e-04	219084	!	AC073812	Mus musculus clone	gb_ba:ASU21853	+	39.00	107.28	1.1e+03	4938	!	U21853	Anabaena sp. phycob1
gb_hhg:AC063968	+	40.00	77.39	4.9e-04	220237	!	AC063968	Mus musculus clone	gb_pr:AB037836	+	39.00	106.36	1.2e+03	5480	!	AB037836	Homo sapiens mRNA
gb_hhg:AC019008	-	40.00	77.20	5.0e-04	224956	!	AC019008	Mus musculus chromo	gb_pr:AB007916	+	39.00	105.66	1.3e+03	5932	!	AB007916	Homo sapiens mRNA
gb_hhg:AC073704	-	40.00	77.12	5.0e-04	226153	!	AC073704	Mus musculus clone	gb_ba:PPFORVOR	+	39.00	101.41	2.3e+03	5985	!	X85250	P.furiosus vorA, vor
gb_hhg:AC060772	+	40.00	77.12	5.0e-04	227074	!	AC060772	Mus musculus clone	gb_ba:AE007818	+	39.00	101.02	2.4e+03	10018	!	AE007818	Thermotoga mariti
gb_ro:AC068561	+	40.00	76.97	5.1e-04	230839	!	AC068561	Mus musculus chromo	gb_ba:AE004815	+	39.00	100.81	2.4e+03	100254	!	AE004815	Pseudomonas aerug
gb_hhg:AC073770	+	40.00	76.94	5.2e-04	231661	!	AC073770	Mus musculus clone	gb_ba:AE005326	+	39.00	100.70	2.5e+03	10382	!	AE005326	Escherichia coli
gb_hhg:AL513352	+	40.00	76.81	5.3e-04	235039	!	AL513352	Mus musculus chromo	gb_ba:AE001865	+	39.00	100.67	2.5e+03	10419	!	AE001865	Deinococcus radio
gb_hhg:AC073791	+	40.00	76.64	5.4e-04	239574	!	AC073791	Mus musculus clone	gb_ba:AE004147	+	39.00	100.31	2.6e+03	10856	!	AE004147	Vibrio cholerae c
gb_hhg:AC051620	+	40.00	76.29	5.6e-04	249433	!	AC051620	Mus musculus clone	gb_ba:AE007818	+	39.00	100.23	2.6e+03	10956	!	AE007818	Clostridium aceto
gb_hhg:AL596255	+	40.00	76.26	5.6e-04	250327	!	AL596255	Mus musculus chromo	gb_ba:AE005011	+	39.00	100.09	2.7e+03	11131	!	AE005011	Halobacterium sp.
gb_hhg:AL591865	+	40.00	76.19	5.7e-04	252137	!	AL591865	Mus musculus chromo	gb_ba:AE004221	+	39.00	99.88	2.8e+03	11401	!	AE004221	Vibrio cholerae c
gb_hhg:AC091548	+	40.00	76.16	5.7e-04	253026	!	AC091548	Mus musculus chromo	gb_ba:U32813	+	39.00	99.66	2.8e+03	11681	!	U32813	Hemophilus influen
gb_pat:AX067466	+	40.00	75.61	6.1e-04	269223	!	AX067466	Sequence 41 from Pa	gb_ba:AE000212	+	39.00	99.61	2.8e+03	11749	!	AE000212	Escherichia coli
gb_pr:AB006639	-	40.00	75.58	6.1e-04	270150	!	AB006639	Homo sapiens genom	gb_ro:AB009371	+	39.00	99.48	2.9e+03	11919	!	AB009371	Mus musculus Tsc2
gb_pr:AB006234	-	40.00	74.65	6.9e-04	300000	!	AB006234	Homo sapiens genom	gb_ba:AE006061	+	39.00	98.72	3.2e+03	12997	!	AE006061	Pasteurella multo
gb_in:AE003453	-	40.00	74.58	7.0e-04	302547	!	AE003453	Drosophila melanoga	gb_ba:AE004466	+	39.00	98.44	3.3e+03	13409	!	AE004466	Pseudomonas aerug
gb_hhg:AC073495	-	40.00	74.11	7.4e-04	318930	!	AC073495	Mus musculus chromo	gb_ba:AE008126	+	39.00	97.72	3.6e+03	14545	!	AE008126	Agrobacterium tum
gb_ba:NM622491	-	40.00	73.91	7.6e-04	326301	!	AL162757	Neisseria meningiti	gb_ba:AE001213	+	39.00	97.55	3.7e+03	14838	!	AE001213	Treponema pallidu
gb_pr:AC016678	+	40.00	73.55	7.9e-04	340000	!	AC016678	Homo sapiens genom	gb_pat:AE191756	+	39.00	97.53	3.7e+03	14838	!	AX191756	Sequence 38 from
gb_hhg:AC025110	+	39.50	84.53	2.0e-04	79685	!	AC025110	Homo sapiens chromo	gb_ba:D90748	+	39.00	97.44	3.8e+03	15007	!	D90748	Escherichia coli ge
gb_hhg:AC073763.2	+	39.50	81.68	2.8e-04	110000	!	Continuation (3 of 4) of AC0		gb_in:AE003364	+	39.00	97.42	3.8e+03	15042	!	AC003364	Drosophila melano
gb_hhg:LMF1CHR16_04	+	39.50	81.68	2.8e-04	110000	!	Continuation (5 of 11) of LM		gb_ov:GGA250458	+	39.00	96.86	4.1e+03	16029	!	AJ250458	Gallus gallus zw1
gb_hhg:AC091362	+	39.50	77.02	5.1e-04	186243	!	AC091362	Rattus norvegicus clone	gb_in:CEV10666G	+	39.00	94.80	5.3e+03	20244	!	AL10470	Streptomyces coel
gb_pr:GHCAD45A	-	39.00	134.04	34.43	240	!	Z27350 G.hirsutum (AD45A) copia		gb_ba:SCF85	-	39.00	94.30	5.6e+03	21420	!	AL10470	Streptomyces coel
gb_pr:GHCAD47	-	39.00	132.12	44.01	298	!	Z27353 G.hirsutum (AD47) copia		gb_ba:SDPFB	-	39.00	93.97	5.9e+03	22233	!	X72850	Sphingomonas sp. dx
gb_om:SSU55958	-	39.00	131.97	44.85	303	!	U55858 Sus scrofa beta 3 adrene		gb_in:LMF15856	+	39.00	93.44	6.3e+03	23600	!	AF17592	Leishmania major
gb_pr:SF9249	-	39.00	130.09	57.13	375	!	S79249 Ig-beta/B29-CD79b (alter		gb_ba:AF179611	+	39.00	89.11	1.2e+04	42703	!	Z81465	Caenorhabditis eleg
gb_pat:AC018071	+	39.00	130.02	57.65	378	!	X83539 H.sapiens B29 mRNA for I		gb_in:CBC099p	+	39.00	88.19	1.2e+04	42703	!	AX015913	Caenorhabditis eleg
gb_ba:AVIFDXA	-	39.00	126.73	87.86	548	!	AR129173 Sequence 19 from Paten		gb_pat:AC036219	+	39.00	85.37	1.8e+04	58779	!	AC036219	Homo sapiens chro
gb_pat:AF159321	+	39.00	125.25	106.27	703	!	AR129173 Sequence 31 from Paten		gb_hhg:AC036219	+	39.00	85.37	1.8e+04	58779	!	AC036219	Homo sapiens chro
gb_hhg:AC129173	+	39.00	124.53	116.56	748	!	AR129173 Sequence 31 from Paten		gb_hhg:AC087185	+	39.00	84.99	1.9e+04	61359	!	AC087185	Homo sapiens chro
gb_hhg:AC051996	+	39.00	122.53	150.58	891	!	AC051996 Giardia intestinalis c		gb_hhg:AL353144	+	39.00	83.72	2.2e+04	70788	!	AL353144	Homo sapiens chro
gb_hhg:AC071566	+	39.00	121.43	173.47	998	!	AC071566 Giardia intestinalis c		gb_hhg:AC036189	+	39.00	83.72	2.2e+04	70788	!	AC036189	Homo sapiens chro
gb_hhg:AC033878	+	39.00	121.41	173.87	1000	!	AC033878 Giardia intestinalis c		gb_hhg:AL359692	+	39.00	82.82	2.5e+04	79376	!	AL359692	Human DNA sequenc
gb_ro:MM0309317	+	39.00	121.34	175.45	1008	!	AC0309317 Mus musculus partial		gb_hhg:AC023239	+	39.00	82.47	2.6e+04	81557	!	AC023239	Mus musculus clon
gb_hhg:AC078596	+	39.00	121.19	178.81	1025	!	AC078596 Giardia intestinalis		gb_pr:AL559397	+	39.00	82.35	2.6e+04	82646	!	AL559397	Human DNA sequenc
gb_hhg:AC071721	+	39.00	121.14	180.00	1031	!	AC071721 Giardia intestinalis		gb_pi:AB013392	+	39.00	82.19	2.7e+04	84129	!	AB013392	Arabidopsis thali
gb_pi:AF155932	+	39.00	121.02	182.77	1045	!	AF155932 Avena sativa 1.3-beta		gb_pr:AC006473	+	39.00	82.03	2.7e+04	85691	!	AC006473	Homo sapiens chro
gb_pat:176270	+	39.00	120.07	206.57	1164	!	I76270 Sequence 3 from patent		gb_pr:AL445470	+	39.00	81.96	2.7e+04	86332	!	AL445470	Human DNA sequenc
gb_ro:BC002181	+	39.00	119.41	224.78	1254	!	BC002181 Mus musculus, clone M		gb_pr:HSA297357	+	39.00	81.85	2.8e+04	87434	!	AJ297357	Homo sapiens part
gb_ro:AF193027	+	39.00	119.18	231.30	1286	!	AF193027 Mus musculus beta-3b		gb_pi:AC004482	+	39.00	81.84	2.8e+04	87509	!	AC004482	Arabidopsis thali
gb_pr:BC002843	+	39.00	118.98	237.43	1316	!	BC002843 Homo sapiens, clone M		gb_hhg:AC005442	+	39.00	81.52	2.9e+04	90788	!	AC005442	Drosophila melano
gb_pat:176271	+	39.00	118.69	246.46	1360	!	I76271 Sequence 4 from patent		gb_hhg:AC07927	+	39.00	81.01	3.1e+04	96132	!	AC07927	Drosophila melano
gb_pi:BC010500	+	39.00	118.31	258.84	1420	!	BC010500 Homo sapiens, clone I		gb_pi:AC002534	+	39.00	80.52	3.3e+04	101371	!	AC002534	Arabidopsis thali
gb_pat:AX151232	+	39.00	116.97	307.33	1652	!	AX151232 Sequence 17 from Paten		gb_pr:AC005018	+	39.00	80.04	3.5e+04	107527	!	AC005018	Homo sapiens BAC
gb_pat:176289	+	39.00	115.64	364.50	1920	!	I76289 Sequence 1 from patent		gb_pi:AC002482	+	39.00	80.00	3.5e+04	107815	!	AC002482	Human BAC clone
gb_pi:MMB3AR	-	39.00	115.64	364.50	1920	!	I76289 Sequence 1 from patent		gb_hhg:AL356434	+	39.00	79.88	3.6e+04	109224	!	AL356434	Homo sapiens chr
gb_pi:BC011045	+	39.00	115.64	364.50	1920	!	I76289 Sequence 1 from patent		gb_pi:HS2828E3	+	39.00	79.77	3.6e+04	110608	!	AL31282	Human DNA sequen
gb_pi:AC001316	+	39.00	114.50	421.88	2193	!	AC001316 Homo sapiens, clone M		gb_hhg:DMR29G2	+	39.00	79.61	3.7e+04	112702	!	AL13487	Drosophila melan
gb_pi:HSB00034	+	39.00	114.46	423.85	2193	!	AC001316 Homo sapiens, clone M		gb_pr:CHNS05TEL	+	39.00	79.42	3.8e+04	115087	!	AL35923	Human chromosome
gb_in:AF332146	+	39.00	113.72	465.98	2384	!	AF332146 Homo sapiens mRNA; cd		gb_pi:AL391803	+	39.00	79.20	3.9e+04	117951	!	AL391803	Human DNA sequen
gb_pi:AK022944	+	39.00	112.09	574.27	2866	!	AK022944 Homo sapiens cDNA FLJ		gb_hhg:AP001482	+	39.00	79.18	3.9e+04	118269	!	AP001482	Homo sapiens chr
gb_pat:AX141241	+	39.00	112.09	574.72	2868	!	AX141241 Sequence 4 from Paten		gb_hhg:AC009829	+	39.00	79.06	3.9e+04	119937	!	AC009829	Homo sapiens chr
gb_pr:AK022397	+	39.00	111.81	595.23	2958	!	AK022397 Homo sapiens cDNA FLJ		gb_hhg:AC014962	+	39.00	78.99	4.0e+04	120829	!	AC014962	Drosophila melan
gb_pi:AK021784	+	39.00	110.90	669.52	3281	!	AK021784 Homo sapiens cDNA FLJ		gb_hhg:AC014962	+	39.00	78.83	4.1e+04	123004	!	AC014962	Drosophila melan
gb_ro:MMB3A	-	39.00	110.48	705.99	3438	!	X72862 M.musculus gene for bet		gb_pi:AL445251	+	39.00	78.76	4.1e+04	123482	!	AL445251	Human DNA sequen
gb_ba:AVIFDXA	-	39.00	110.4														

gb_htg:AC034267	131980	4.4e+04	78.21	39.00	-	AC034267 Homo sapiens chrom	gb_htg:AC018665	186632	6.5e+04	75.14	39.00	AC018665 Homo sapiens chr
gb_htg:AC090880	133520	4.5e+04	78.11	39.00	-	AC090880 Mus musculus clone	gb_htg:AC093353	187614	6.5e+04	75.10	39.00	AC093353 Mus musculus clo
gb_htg:AC091502	138221	4.6e+04	77.80	39.00	-	AC091502 Rattus norvegicus c	gb_pr:AC006369	188359	6.6e+04	75.06	39.00	AC006369 Homo sapiens BAC
gb_htg:AL592525	143068	4.8e+04	77.50	39.00	+	AL592525 Homo sapiens chrom	gb_htg:AC022546	188781	6.6e+04	75.04	39.00	AC022546 Homo sapiens chr
gb_htg:AC068266	149235	5.0e+04	77.12	39.00	+	AC068266 Homo sapiens chrom	gb_htg:AC067817	189027	6.6e+04	75.03	39.00	AC067817 Homo sapiens chr
gb_htg:AL160169	149356	5.1e+04	77.11	39.00	+	AL160169 Homo sapiens chrom	gb_htg:AC019142	189036	6.6e+04	75.03	39.00	AC019142 Homo sapiens chr
gb_htg:AL596257	154145	5.1e+04	76.96	39.00	+	AL596257 Homo sapiens chrom	gb_htg:AL596265	189135	6.6e+04	75.03	39.00	AL596265 Mus musculus chr
gb_pr:AC068722	154194	5.2e+04	76.99	39.00	+	AC068722 Homo sapiens chrom	gb_htg:AC011193	189319	6.6e+04	75.02	39.00	AC011193 Homo sapiens chr
gb_htg:AC091620	152906	5.2e+04	76.91	39.00	+	AC091620 Papio cynocephalus	gb_htg:AC079270	189709	6.6e+04	75.00	39.00	AC079270 Homo sapiens chr
gb_htg:AC011974	153202	5.2e+04	76.89	39.00	+	AC011974 Homo sapiens clone	gb_pr:AC010745	189894	6.6e+04	74.99	39.00	AC010745 Homo sapiens BAC
gb_htg:AC087262	154441	5.2e+04	76.82	39.00	+	AC087262 Rattus norvegicus c	gb_htg:AC021177	190488	6.6e+04	74.96	39.00	AC021177 Homo sapiens chr
gb_ba:D90917	154619	5.3e+04	76.81	39.00	+	D90917 Synecocystis sp. FCC	gb_htg:AC000491	192000	6.7e+04	74.89	39.00	AC000491 Mus musculus chr
gb_htg:AC009271	155157	5.3e+04	76.78	39.00	+	AC009271 Homo sapiens chrom	em_htg:hum:AC0073505	193261	6.8e+04	74.83	39.00	AC0073505 Homo sapiens chr
gb_pr:CNS01DWF	155742	5.3e+04	76.74	39.00	+	AL137190 Human chromosome 14	gb_htg:AC024545	193700	6.8e+04	74.81	39.00	AC024545 Homo sapiens clo
gb_pr:AC051TEG	157577	5.4e+04	76.64	39.00	+	AL1359212 Human chromosome 14	gb_htg:AC013775	194609	6.8e+04	74.77	39.00	AC013775 Mus musculus clo
gb_htg:AP003443	160579	5.5e+04	76.47	39.00	+	AP003443 Oryza sativa chrom	gb_htg:AL590430	195107	6.8e+04	74.75	39.00	AL590430 Mus musculus chr
gb_htg:AC023586	160569	5.5e+04	76.47	39.00	+	AC023586 Homo sapiens chrom	AC079419	196003	6.8e+04	74.71	39.00	AC079419 Mus musculus chr
gb_pr:AC090937	160596	5.5e+04	76.47	39.00	+	AC090937 Homo sapiens chrom	AL117346	196247	6.9e+04	74.70	39.00	AL117346 Homo sapiens chr
gb_pr:AC008511	160770	5.5e+04	76.46	39.00	+	AC008511 Homo sapiens chrom	AL359176	197195	6.9e+04	74.66	39.00	AL359176 Homo sapiens chr
gb_htg:AC026007	162408	5.6e+04	76.37	39.00	+	AC026007 Homo sapiens chrom	AC010097	198278	6.9e+04	74.61	39.00	AC010097 Homo sapiens chr
gb_pr:AC016574	163183	5.6e+04	76.33	39.00	+	AC016574 Homo sapiens chrom	AL591436	198780	7.0e+04	74.59	39.00	AL591436 Mus musculus chr
gb_htg:AC026761	164513	5.6e+04	76.26	39.00	+	AC026761 Mus musculus chrom	AL353729	199762	7.0e+04	74.54	39.00	AL353729 Homo sapiens chr
gb_pr:HSJ29318	164808	5.6e+04	76.24	39.00	+	AL078594 Human DNA sequence	AC092797	200911	7.1e+04	74.49	39.00	AC092797 Homo sapiens chr
gb_htg:AL535093	164845	5.6e+04	76.24	39.00	+	AL535093 Homo sapiens chrom	AC079442	201289	7.1e+04	74.47	39.00	AC079442 Mus musculus chr
gb_pr:CNS01DWC	166486	5.7e+04	76.15	39.00	+	AL137100 Human chromosome 14	AL591706	201725	7.1e+04	74.46	39.00	AL591706 Homo sapiens chr
gb_htg:AC025318	166678	5.7e+04	76.14	39.00	+	AC025318 Homo sapiens chrom	gb_pr:CNS05TCL	201844	7.1e+04	74.45	39.00	AL355102 Human chromosome
gb_htg:AC026165	167277	5.7e+04	76.11	39.00	+	AC026165 Homo sapiens chrom	gb_htg:AC051963	201852	7.1e+04	74.45	39.00	AC051963 Mus musculus chr
gb_pr:AC079468	167656	5.8e+04	76.09	39.00	+	AC079468 Homo sapiens chrom	gb_htg:AL596117	202362	7.1e+04	74.43	39.00	AL596117 Mus musculus chr
gb_htg:AC053483	168332	5.8e+04	76.06	39.00	+	AC053483 Homo sapiens chrom	gb_ro:AC021667	203106	7.1e+04	74.37	39.00	AC021667 Mus musculus cl
gb_htg:AC062007	168466	5.8e+04	76.05	39.00	+	AC062007 Homo sapiens chrom	gb_htg:AC021445	203621	7.2e+04	74.37	39.00	AC021445 Mus musculus clo
gb_pr:AC013463	168493	5.8e+04	76.05	39.00	+	AC013463 Homo sapiens chrom	gb_ro:AC079644	204394	7.2e+04	74.32	39.00	AC079644 Mus musculus 12
gb_htg:AC051597	169102	5.8e+04	76.02	39.00	+	AL359997 Human DNA sequence	AC010359	204943	7.2e+04	74.32	39.00	AC010359 Homo sapiens chr
gb_htg:AC091503	169514	5.8e+04	75.99	39.00	+	AC091503 Rattus norvegicus c	AC087227	205691	7.2e+04	74.28	39.00	AC087227 Mus musculus chr
gb_pr:AC064869	169514	5.8e+04	75.99	39.00	+	AC064869 Homo sapiens clone	AC044847	205910	7.2e+04	74.27	39.00	AC044847 Mus musculus chr
gb_htg:AC016481	169913	5.8e+04	75.97	39.00	+	AC016481 Homo sapiens clone	AC087135	209958	7.4e+04	74.10	39.00	AC087135 Mus musculus clo
gb_htg:AC069447	170105	5.9e+04	75.96	39.00	+	AC069447 Mus musculus chrom	AL590614	211033	7.5e+04	74.06	39.00	AL590614 Mus musculus chr
gb_htg:AC062736	170186	5.9e+04	75.96	39.00	+	AC062736 Homo sapiens chrom	AC013368	211967	7.5e+04	74.02	39.00	AC013368 Homo sapiens clo
gb_in:AC009250	170362	5.9e+04	75.95	39.00	+	AC009250 Drosophila melanog	AC073883	212987	7.5e+04	73.97	39.00	AC073883 Mus musculus chr
gb_htg:AC092045	171321	5.9e+04	75.90	39.00	+	AC092045 Homo sapiens chrom	AC093339	215352	7.6e+04	73.88	39.00	AC093339 Mus musculus clo
em_htg:hum:AC024148	172033	5.9e+04	75.86	39.00	+	AC024148 Homo sapiens chrom	AL592547	216016	7.6e+04	73.85	39.00	AL592547 Mus musculus chr
gb_htg:AL442004	172219	5.9e+04	75.85	39.00	+	AL442004 Homo sapiens chrom	AC034265	218205	7.7e+04	73.76	39.00	AC034265 Mus musculus chr
gb_htg:AL591127	172385	5.9e+04	75.85	39.00	+	AL591127 Mus musculus chrom	AC083890	218270	7.8e+04	73.76	39.00	AC083890 Mus musculus chr
gb_ro:CNS07EGP	172751	6.0e+04	75.83	39.00	+	AL591826 BAC 13C18 of librar	AC087556	220460	7.8e+04	73.73	39.00	AC087556 Mus musculus chr
gb_htg:AC013729	173327	6.0e+04	75.80	39.00	+	AC013729 Homo sapiens chrom	gb_htg:AC088356	220605	7.9e+04	73.67	39.00	AC088356 Escherichia coli
gb_pr:AC002360	173379	6.0e+04	75.79	39.00	+	AP002360 Homo sapiens genom	gb_ba:AP002555	222605	8.0e+04	73.58	39.00	AP002555 Homo sapiens chr
gb_pr:CNS05OTC	173389	6.0e+04	75.79	39.00	+	AL355103 Human chromosome 14	gb_htg:AL358779	225022	8.0e+04	73.49	39.00	AL358779 Homo sapiens chr
gb_htg:AC068960	173975	6.0e+04	75.76	39.00	+	AC068960 Homo sapiens chrom	AC027281	225157	8.0e+04	73.48	39.00	AC027281 Homo sapiens chr
gb_pr:AC011841	174588	6.0e+04	75.73	39.00	+	AC011841 Homo sapiens chrom	gb_htg:AC073680	226013	8.0e+04	73.45	39.00	AC073680 Mus musculus clo
gb_htg:AC023889	174612	6.0e+04	75.73	39.00	+	AC023889 Homo sapiens chrom	AC091287	227518	8.1e+04	73.39	39.00	AC091287 Mus musculus clo
gb_htg:AC073748	175371	6.1e+04	75.69	39.00	+	AC073748 Mus musculus clone	AC090652	228159	8.1e+04	73.37	39.00	AC090652 Mus musculus clo
AC027619	175399	6.1e+04	75.69	39.00	+	AC027619 Homo sapiens chrom	gb_htg:AC090122	229774	8.2e+04	73.30	39.00	AC090122 Mus musculus clo
em_htg:hum:AC012036	177341	6.1e+04	75.60	39.00	+	AC012036 Homo sapiens chrom	gb_vl:AF232689	229996	8.2e+04	73.30	39.00	AF232689 Rat cytomegalovi
gb_htg:AC032013	177421	6.1e+04	75.59	39.00	+	AC032013 Mus musculus chrom	gb_htg:AC073691	231443	8.3e+04	73.24	39.00	AC073691 Mus musculus clo
gb_htg:AC079443	177809	6.1e+04	75.57	39.00	+	AC079443 Mus musculus chrom	AC079638	231861	8.3e+04	73.20	39.00	AC079638 Mus musculus clo
gb_htg:AC025163	177876	6.2e+04	75.57	39.00	+	AC025163 Homo sapiens chrom	gb_htg:AC092254	238637	8.6e+04	72.97	39.00	AC092254 Mus musculus clo
gb_htg:AC080155	177924	6.2e+04	75.57	39.00	+	AC080155 Rattus norvegicus c	gb_htg:AC044892	240294	8.6e+04	72.91	39.00	AC044892 Homo sapiens chr
gb_htg:AC087869	178032	6.2e+04	75.56	39.00	+	AC087869 Mus musculus clone	gb_htg:AL360154	240579	8.6e+04	72.90	39.00	AL360154 Homo sapiens chr
gb_htg:AC026626	178953	6.2e+04	75.51	39.00	+	AC026626 Homo sapiens chrom	gb_htg:AL589661	241226	8.7e+04	72.87	39.00	AL589661 Mus musculus chr
AC010178	179070	6.2e+04	75.51	39.00	+	AC010178 Homo sapiens chrom	gb_htg:AC025909	242899	8.9e+04	72.63	39.00	AC025909 Mus musculus chr
gb_pr:AC016643	179969	6.2e+04	75.46	39.00	+	AC016643 Homo sapiens chrom	gb_in:AE003653	249469	9.0e+04	72.58	39.00	AE003653 Drosophila melan
gb_htg:AP003766	180865	6.3e+04	75.42	39.00	+	AP003766 Oryza sativa chrom	gb_htg:AC073677	251579	9.1e+04	72.50	39.00	AC073677 Mus musculus clo
gb_htg:AC062006	181062	6.3e+04	75.41	39.00	+	AC062006 Homo sapiens chrom	gb_htg:AC073677	251579	9.1e+04	72.50	39.00	AC073677 Mus musculus clo
gb_htg:AC072057	181452	6.3e+04	75.39	39.00	+	AC072057 Homo sapiens chrom	gb_ba:AP000007	253505	9.1e+04	72.43	39.00	AP000007 Pyrococcus horik
gb_htg:AC025878	182204	6.3e+04	75.36	39.00	+	AC025878 Homo sapiens clone	gb_htg:AL513124	261141	9.5e+04	72.17	39.00	AL513124 Homo sapiens chr
gb_htg:AL592464	182766	6.3e+04	75.33	39.00	+	AL592464 Homo sapiens chrom	AC087228	265537	9.6e+04	72.02	39.00	AC087228 Mus musculus chr
gb_htg:AC040980	183150	6.4e+04	75.31	39.00	+	AC040980 Homo sapiens chrom	AC087129	266574	9.7e+04	71.99	39.00	AC087129 Mus musculus clo
gb_htg:AP002000	183197	6.4e+04	75.31	39.00	+	AP002000 Homo sapiens chrom	AC068493	269081	9.8e+04	71.91	39.00	AC068493 Mus musculus clo
gb_htg:AC068828	183487	6.4e+04	75.29	39.00	+	AC068828 Homo sapiens clone	AC092180	272120	9.9e+04	71.81	39.00	AC092180 Homo sapiens chr
gb_pr:AC020709	184104	6.4e+04	75.26	39.00	+	AC020709 Homo sapiens clone	AL590968	272351	9.9e+04	71.80	39.00	AL590968 Mus musculus chr
gb_htg:AC025861	185143	6.4e+04	75.21	39.00	+	AC025861 Homo sapiens clone	gb_in:AE003542	289887	1.1e+05	71.25	39.00	AE003542 Sirophobium melan
gb_htg:AC090734	185272	6.4e+04	75.21	39.00	+	AC090734 Homo sapiens chrom	gb_ba:SNES051789	294800	1.1e+05	71.10	39.00	AE051789 Drosophila
gb_htg:AC069253	185580	6.5e+04	75.19	39.00	+	AC069253 Homo sapiens chrom	gb_htg:AC092369	302015	1.1e+05	70.88	39.00	AC092369 Homo sapiens chr
gb_htg:AC073420	186349	6.5e+04	75.16	39.00	+	AC073420 Homo sapiens chrom	gb_ba:GJ11168X1	314150	1.2e+05	70.54	39.00	AL139074 Campylobacter je

gb_hcg:AL356291	39.00	70.44	1.2e+05	317436	! AL356291 Homo sapiens chromo	gb_ba:AE004227	38.00	97.17	3.9e+03	10177	! AE004227 Vibrio cholerae c
gb_hcg:AC010277	39.00	70.26	1.2e+05	324165	! AC010277 Homo sapiens chromo	gb_ba:AE001922	38.00	96.97	4.0e+03	10410	! AE001922 pseudococcus radio
gb_ba:AP003005	39.00	70.03	1.2e+05	332635	! AP003005 Mesorhizobium loti	gb_ba:AE004595	38.00	96.94	4.0e+03	10448	! AE004595 pseudomonas aerug
gb_ba:AP003010	39.00	69.81	1.3e+05	340857	! AP003010 Mesorhizobium loti	gb_ba:AE004618	38.00	96.43	4.3e+03	11060	! AE004618 pseudomonas aerug
gb_ba:AP003095	39.00	69.66	1.3e+05	346897	! AP003095 Mesorhizobium loti	gb_pi:SPAC32A11	38.00	96.17	4.4e+03	11401	! 269796 S.pombe chromosome
gb_ba:AP003007	39.00	69.62	1.3e+05	348411	! AP003007 Mesorhizobium loti	gb_ba:AE005669	38.00	96.01	4.5e+03	11599	! AE005669 Escherichia coli
gb_ba:AE005019	38.50	72.83	3.1e+04	10156	! AE005019 Halobacterium sp. NR	gb_ba:AE000148	38.00	95.94	4.6e+03	11692	! AE000148 Escherichia coli
gb_hcg:AC073146	38.50	72.83	3.1e+04	136646	! AC073146 Homo sapiens chromo	gb_ba:AE005221	38.00	95.83	4.6e+03	11845	! AE005221 Escherichia coli
gb_sts:G28085	38.00	125.10	1.0e+04	433	! G28085 human STS SHGC-33555, se	gb_hcg:AC020143	38.00	95.82	4.6e+03	11854	! AC020143 Streptomyces gris
gb_ba:BBU91793	38.00	122.94	142.87	553	! BBU91793 Borrelia burgdorferi str	gb_ba:AB011413	38.00	95.66	4.7e+03	12070	! AB011413 Streptomyces gris
gb_ba:BOR220SPC	38.00	122.72	146.98	567	! BOR220SPC Borrelia burgdorferi (st	gb_ba:AE000769	38.00	95.31	4.9e+03	12563	! AE000769 Aquifex aeolicus
gb_ba:BGOSPC1	38.00	121.87	163.86	657	! BGOSPC1 B.garini (strain Tsi1)	gb_ba:AE0005970	38.00	95.23	5.0e+03	12680	! AE0005970 Caulobacter cresc
gb_hcg:AC051422	38.00	121.42	173.73	657	! AC051422 Giardia intestinalis c	gb_ba:AE0004759	38.00	94.16	5.7e+03	13409	! AE0004759 Pseudomonas aerug
gb_sts:G73117	38.00	121.28	173.73	667	! G73117 MARC 7899-7900:99688143	gb_ba:AE006848	38.00	93.88	5.9e+03	14759	! AE006848 Sulfolobus solfat
gb_ro:MUSIGG4014	38.00	120.83	187.29	702	! MUSIGG4014 Mus musculus rearranged	gb_pi:AC093181	38.00	93.68	6.1e+03	15101	! AC093181 Sequence 14 from
gb_pat:105395	38.00	119.97	209.24	774	! 105395 Sequence 2 from Patent E	gb_pat:AC26843	38.00	93.68	6.1e+03	15108	! AC26843 Lelystad Agent-spec
gb_pi:HSX13782	38.00	119.97	209.24	774	! HSX13782 Homo sapiens mRNA for te	gb_pi:AR137155	38.00	93.68	6.1e+03	15108	! AR137155 Sequence 1 from p
gb_pat:AX056449	38.00	119.43	224.02	822	! AX056449 Sequence 93 from Patent	gb_pat:140237	38.00	93.68	6.1e+03	15108	! 140237 Sequence 1 from pat
gb_hcg:AC0190530	38.00	119.42	224.33	823	! AC0190530 Sequence 1 from Patent	gb_pi:LEYPOLYENV	38.00	93.67	6.1e+03	15111	! LEYPOLYENV Methanobacterium
gb_hcg:AC037791	38.00	118.83	242.04	880	! AC037791 Giardia intestinalis c	gb_ba:AE000934	38.00	93.67	6.1e+03	15124	! AE000934 Methanobacterium
gb_hcg:AC038802	38.00	118.44	254.57	920	! AC038802 Giardia intestinalis c	gb_hcg:AC090678	38.00	93.60	6.2e+03	15239	! AC090678 Homo sapiens chro
gb_hcg:AC076604	38.00	118.42	255.19	922	! AC076604 Giardia intestinalis c	gb_ba:AE005026	38.00	93.53	6.2e+03	15355	! AE005026 Halobacterium sp.
gb_hcg:AC080544	38.00	118.31	258.65	933	! AC080544 Giardia intestinalis c	gb_ba:AE000508	38.00	93.44	6.3e+03	15518	! AE000508 Escherichia coli
gb_ba:BORVMD2A	38.00	118.06	267.16	960	! BORVMD2A Borrelia hermsi outer m	gb_ba:AE004094	38.00	93.08	6.6e+03	16164	! AE004094 Vibrio cholerae c
gb_hcg:AC062559	38.00	118.05	267.48	961	! AC062559 Giardia intestinalis c	gb_hcg:AC017330	38.00	92.80	6.8e+03	16673	! AC017330 Drosophila melano
gb_hcg:AC051183	38.00	117.91	272.22	976	! AC051183 Giardia intestinalis c	gb_ba:AE0007029	38.00	92.48	7.1e+03	17286	! AE0007029 Mycobacterium tub
gb_pi:AF217397	38.00	117.87	273.80	981	! AF217397 Drosophila melanogaste	gb_pi:MTBL1	38.00	92.16	7.4e+03	17334	! MTBL1 Mycobacterium tuber
gb_hcg:AC051094	38.00	116.82	313.08	1104	! AC051094 Giardia intestinalis	gb_ba:BSGTHR2	38.00	91.25	8.3e+03	19861	! BSGTHR2 S.pombe chromosom
gb_pat:AX143781	38.00	115.65	363.74	1260	! AX143781 Sequence 1 from Patent	gb_pi:SPAC750	38.00	89.47	1.0e+04	24290	! SPAC750 S.pombe chromosom
gb_ro:AF329484	38.00	115.20	385.76	1327	! AF329484 Mus musculus serine/t	gb_pi:SCD12A	38.00	87.41	1.4e+04	30657	! SCD12A Streptomyces coel
gb_pi:DROGABARS	38.00	114.16	440.30	1491	! DROGABARS Drosophila melanogaster	gb_ba:SC8EA4	38.00	86.74	1.5e+04	33084	! SC8EA4 Streptomyces coel
gb_pi:SG2717	38.00	114.16	440.30	1491	! SG2717 LCCH3-putative gamma-am	gb_ba:MTCY01B2	38.00	86.01	1.6e+04	35938	! MTCY01B2 Mycobacterium tuber
gb_pat:AC068511	38.00	114.16	440.30	1491	! AC068511 Sequence 1 from patent	gb_hcg:AC014499	38.00	85.76	1.7e+04	36948	! AC014499 Drosophila melano
gb_pi:117317	38.00	114.16	440.30	1491	! 117317 Sequence 3 from patent	gb_pi:SPAC56F8	38.00	85.73	1.7e+04	37093	! SPAC56F8 S.pombe chromosom
gb_pat:AX141289	38.00	113.85	458.44	1545	! AX141289 Sequence 11 from Paten	gb_hcg:AC080114	38.00	85.66	1.7e+04	37367	! AC080114 Homo sapiens chro
gb_pi:AF329483	38.00	113.80	461.47	1554	! AF329483 Homo sapiens serine/t	gb_pi:SPAC1348	38.00	85.24	1.8e+04	39187	! SPAC1348 S.pombe chromosom
gb_pi:AF149214	38.00	113.78	462.82	1558	! AF149214 Rattus norvegicus pro	gb_pi:SPAC977	38.00	84.88	1.9e+04	40815	! SPAC977 S.pombe chromosom
gb_pi:AF149215	38.00	113.78	462.82	1558	! AF149215 Rattus norvegicus pro	gb_pi:CBG45N02	38.00	84.48	2.0e+04	42726	! CBG45N02 Caenorhabditis br
gb_pi:AF149216	38.00	113.78	462.82	1558	! AF149216 Rattus norvegicus pro	gb_pi:AC007206	38.00	84.48	2.0e+04	42732	! AC007206 Homo sapiens chro
gb_pi:AF149217	38.00	113.78	462.82	1558	! AF149217 Rattus norvegicus pro	gb_pi:AC019872	38.00	84.08	2.1e+04	44671	! AC019872 Drosophila melano
gb_pi:AF149218	38.00	113.78	462.82	1558	! AF149218 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149219	38.00	113.78	462.82	1558	! AF149219 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149220	38.00	113.78	462.82	1558	! AF149220 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149221	38.00	113.78	462.82	1558	! AF149221 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149222	38.00	113.78	462.82	1558	! AF149222 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149223	38.00	113.78	462.82	1558	! AF149223 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149224	38.00	113.78	462.82	1558	! AF149224 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149225	38.00	113.78	462.82	1558	! AF149225 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149226	38.00	113.78	462.82	1558	! AF149226 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149227	38.00	113.78	462.82	1558	! AF149227 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149228	38.00	113.78	462.82	1558	! AF149228 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149229	38.00	113.78	462.82	1558	! AF149229 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149230	38.00	113.78	462.82	1558	! AF149230 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149231	38.00	113.78	462.82	1558	! AF149231 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149232	38.00	113.78	462.82	1558	! AF149232 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149233	38.00	113.78	462.82	1558	! AF149233 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149234	38.00	113.78	462.82	1558	! AF149234 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149235	38.00	113.78	462.82	1558	! AF149235 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149236	38.00	113.78	462.82	1558	! AF149236 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149237	38.00	113.78	462.82	1558	! AF149237 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149238	38.00	113.78	462.82	1558	! AF149238 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
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gb_pi:AF149240	38.00	113.78	462.82	1558	! AF149240 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149241	38.00	113.78	462.82	1558	! AF149241 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
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gb_pi:AF149244	38.00	113.78	462.82	1558	! AF149244 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149245	38.00	113.78	462.82	1558	! AF149245 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
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gb_pi:AF149248	38.00	113.78	462.82	1558	! AF149248 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149249	38.00	113.78	462.82	1558	! AF149249 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149250	38.00	113.78	462.82	1558	! AF149250 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
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gb_pi:AF149252	38.00	113.78	462.82	1558	! AF149252 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
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gb_pi:AF149255	38.00	113.78	462.82	1558	! AF149255 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+04	44986	! AC019806 Drosophila melano
gb_pi:AF149256	38.00	113.78	462.82	1558	! AF149256 Rattus norvegicus pro	gb_pi:AC019806	38.00	84.02	2.1e+		

gb_htg:AC091288_1	-	38.00	76.11	5.7e+04	110000	Continuation (2 of 4) of AC091288_1	gb_htg:AC008336	+	38.00	72.61	8.9e+04	163378	AC008336	Drosophila melan
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gb_htg:AL139143	+	38.00	75.96	5.9e+04	111862	AL139143 Homo sapiens chrom	gb_htg:AC025505	+	38.00	72.43	9.1e+04	166695	AC025505	Homo sapiens chr
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gb_pl:AF275345	-	38.00	75.43	6.3e+04	118813	AF275345 Lycopersicon esculentum	gb_in:AC007471	-	38.00	72.33	9.3e+04	168601	AC007471	Drosophila melan
gb_htg:AC010112	-	38.00	75.19	6.5e+04	122073	AC010112 Drosophila melanogaster	gb_ba:AP002569	-	38.00	72.32	9.3e+04	168764	AP002569	Escherichia coli
gb_htg:AL161737	+	38.00	75.16	6.5e+04	122493	AL161737 Homo sapiens chrom	gb_pr:HS490024	+	38.00	72.32	9.3e+04	168778	AL117338	Human DNA sequen
gb_pr:HSBQ17A99	+	38.00	75.09	6.5e+04	123454	AL450226 Homo sapiens chrom	gb_htg:AC024288	+	38.00	72.28	9.3e+04	169540	AC024288	Homo sapiens chr
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 KEYWORDS
 SOURCE bread wheat.
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.

REFERENCE
 AUTHORS Harberd,N.P. and Peng,J.
 TITLE Genetic control of plant growth and development
 JOURNAL Patent: WO 9909174-A 105 25-FEB-1999;

FEATURES
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 LOCUS AX005857 453 bp DNA 24-AUG-2000
 DEFINITION Sequence 66 from Patent WO9909174.
 ACCESSION AX005857
 VERSION AX005857.1 GI:9928852
 KEYWORDS
 SOURCE bread wheat.
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.

REFERENCE
 AUTHORS Harberd,N.P. and Peng,J.
 TITLE Genetic control of plant growth and development
 JOURNAL Patent: WO 9909174-A 66 25-FEB-1999;

FEATURES
 source Location/Qualifiers
 1..453
 /organism="Triticum aestivum"
 /db_xref="taxon:4565"
 misc_feature
 6 /note="n is any nucleotide"
 misc_feature
 11 /note="n is any nucleotide"
 misc_feature
 46 /note="n is any nucleotide"
 misc_feature
 85 /note="n is any nucleotide"
 misc_feature
 107 /note="n is any nucleotide"
 misc_feature
 445 /note="n is any nucleotide"
 misc_feature
 449 /note="n is any nucleotide"
 BASE COUNT 85 a 136 c 158 g 67 t 7 others
 ORIGIN

alignment_scores:
 Quality: 81.00 Length: 17
 Ratio: 4.765 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-485-529-104 x AX005857 ..

Align seg 1/1 to: AX005857 from: 1 to: 453

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
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 273 GAGGAGCTGTCGGCGCTCGGGTACAGGTGCGCGCTCCGACATGGC 322

17 a 17

|

323 G 323

seq_name: gb_pl:TAE242531

seq_documentation_block:
 LOCUS TAE242531 1872 bp DNA PLN 28-JUL-1999
 DEFINITION Triticum aestivum rht-Dla gene for gibberellin response modulator.
 ACCESSION AJ242531
 VERSION AJ242531.1 GI:5640156
 KEYWORDS gibberellin response modulator; rht-Dla gene.
 SOURCE bread wheat.
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Triticum.
 1 (bases 1 to 1872)
 Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M.,
 Flintham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pelica,F.,
 Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P.
 'Green revolution' genes encode mutant gibberellin response
 modulators
 Nature 400 (6741), 256-261 (1999)

2 (bases 1 to 1872)

99347734

REFERENCE

AUTHORS Harberd,N.P., Peng,J. and Richards,D.E.

TITLE Green revolution genes encode mutant gibberellin response

JOURNAL

MEDLINE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

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source
1..1872
/organism="Triticum aestivum"
/db_xref="taxon:4565"
1..1872
/gene="rht-D1a"
1..1872
/note="GAI ortholog"
/codon_start=1
/product="gibberellin response modulator"
/protein_id="CAB51555.1"
/db_xref="GI:5640157"
/translation="MKREYQDAGSGGGGSGGSEKMMVSAAGEEYDELLAAL
GYKVRASMDADVQKLEAMGMGGVAGAAPDDSPATHLATDTVHYNPTDLSSWV
ESMLSELNADPPPLPPALQNASTSTVTGSGGYEDLPPSDSSSIYALRPISPAG
ATAPADLSADSVRDKRMTGSGTSSSSSSSLGGGARSVVEAAPVAAANATP
ALPVVVDQAGIRLHVALLACAEAVQDENLSAEALVKQIPLLAASQGGAMRKVAA
YFGALARRVFRFPQDSSLLDAADFLLHAHYESCPLYKFAHFTANOAILLAFAG
CRRVHVDGFKQGMQWPAALQALALRPGPESFLTGVPQPDETDALQQVWKLKLA
QFAHTIRVDFOYRGLVAATLADLEPMLQPEGEDPNEPEVIAVNSVFEMHLLAOP
GALEKVLGTVAVRPRIVTVVEQANHNSGTFLDRFTESLHYSTMEDSLGGSGGG
PSEVSSGAAAPAAAGIDQVMSEVYLGROIQCNVACGAERTERHETLQQRNRLGNA
GFETVHLGNSNAYKQASTLLALFAGDGGYKVEEGCLTLGLWHTRLPLIATSAWRLAGP"
BASE COUNT 265 a 700 c 641 g 266 t
ORIGIN

alignment_scores:
  Quality: 81.00 Length: 17
  Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-485-529-104 x TAE242531 ..
Align seg 1/1 to: TAE242531 from: 1 to: 1872

1 AspCluleuLeuAlaLaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
112 GACGAGCTGCTGGCGGCTCGGGTACAGGTGGCGCCCTCCGACATGGC 161

17 a 17
1
162 G 162

seq_name: gb_pat:AX005805

seq_documentation_block:
LOCUS AX005805 2125 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 14 from Patent WO9909174.
ACCESSION AX005805
VERSION AX005805.1 GI:9928802
KEYWORDS
SOURCE
bread wheat.
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 2125)
AUTHORS
Harberd,N.P. and Peng,J.
TITLE
Genetic control of plant growth and development
JOURNAL
Patent: WO 9909174-A 14 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source
1..2125
/organism="Triticum aestivum"
/db_xref="taxon:4565"
misc_feature
6 /note="n is any nucleotide"
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11 /note="n is any nucleotide"
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46 /note="n is any nucleotide"
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107 /note="n is any nucleotide"
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misc_feature
727 /note="n is any nucleotide"
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misc_feature
1444 /note="n is any nucleotide"

BASE COUNT 325 a 768 c 723 g 309 t
ORIGIN

alignment_scores:
  Quality: 81.00 Length: 17
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misc_feature      /note="n is any nucleotide"
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/note="n is any nucleotide"
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1808
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1900
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1940
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1982
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2681
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2689
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2706
/note="n is any nucleotide"
31 others
BASE COUNT      473 a 900 c 823 g 482 t
ORIGIN

alignment_scores:
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Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-485-529-104 x AX005794 ..
Align seg 1/1 to: AX005794 from: 1 to: 2709

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
273 GACGAGCTGCTGGCGCGCTCGGTACAAGTGCCTCGCATGGC 322

17 a 17
323 G 323

seq_name: gb_pat:AX005807

seq_documentation_block: 302 bp DNA PAT 24-AUG-2000
LOCUS AX005807
DEFINITION Sequence 16 from Patent WO9909174.
ACCESSION AX005807
VERSION AX005807.1 GI:9928804
KEYWORDS
SOURCE
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 302)
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 16 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 52 a 82 c 123 g 45 t
ORIGIN
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  Quality: 78.00      Length: 17
  Ratio: 4.588       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x AX005807 ..
Align seg 1/1 to: AX005807 from: 1 to: 302

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
100 GATGAGCTGCTGGCGCGCTCGGTACAAGTGCCTCGCATGGC 149

17 a 17
150 G 150

seq_name: gb_pat:AX005808

seq_documentation_block: 371 bp DNA PAT 24-AUG-2000
LOCUS AX005808
DEFINITION Sequence 17 from Patent WO9909174.
ACCESSION AX005808
VERSION AX005808.1 GI:9928805
KEYWORDS
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 371)
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 17 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source
/organism="Zea mays"
/db_xref="taxon:4577"
BASE COUNT 56 a 121 c 139 g 55 t
ORIGIN

alignment_scores:
  Quality: 78.00      Length: 17
  Ratio: 4.588       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x AX005808 ..
Align seg 1/1 to: AX005808 from: 1 to: 371

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
64 GATGAGCTGCTGGCGCGCTCGGTACAAGTGCCTCGCATGGC 113

17 a 17
114 G 114

seq_name: gb_pat:AX005803

seq_documentation_block: 770 bp DNA PAT 24-AUG-2000
LOCUS AX005803
DEFINITION Sequence 12 from Patent WO9909174.
ACCESSION AX005803
VERSION AX005803.1 GI:9928800
KEYWORDS
SOURCE Oryza sativa.
```

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ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS      Harberd,N.P. and Peng,J.
TITLE        Genetic control of plant growth and development
JOURNAL      Patent: WO 9909174-A 12 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source       Location/Qualifiers
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BASE COUNT   104 a 252 c 294 g 120 t
ORIGIN
alignment_scores
  Quality:   78.00      Length:   17
  Ratio:     4.588      Gaps:     0
  Percent Similarity: 100.000      Percent Identity: 94.118
alignment_block:
US-09-485-529-104 x AX005803      ..
Align seg 1/1 to: AX005803 from: 1 to: 770
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
114 GACGAGCTGCTGGCGGCGCTCGGTACAAAGTGGCGTCCGACATGGC 163
17 a 17
|
164 C 164
seq_name: gb_pl:ZMA242530
seq_documentation_block:
LOCUS      ZMA242530      1890 bp      DNA      28-JUL-1999
DEFINITION Zea mays partial d8 gene for gibberellin response modulator.
ACCESSION   AJ242530
VERSION     AJ242530.1 GI:5640154
KEYWORDS    D8 gene; gibberellin response modulator.
SOURCE      Zea mays.
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M.,
Flintham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pellica,F.,
Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P.
TITLE        'Green revolution' genes encode mutant gibberellin response
modulators
JOURNAL      Nature 400 (6741), 256-261 (1999)
MEDLINE      99347734
REFERENCE    2 (bases 1 to 1890)
AUTHORS      Richards,D.E.
TITLE        Direct Submission
JOURNAL      Submitted (25-MAY-1999) Richards D.E., Molecular Genetics, John
Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
FEATURES
source       Location/Qualifiers
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            /gene="d8"
            1..>1890
            /gene="d8"
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            /codon_start=1
            /product="gibberellin response modulator"
            /protein_id="CAB51557.1"

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/db_xref="GI:5640155"
/translat="MKREYQDAGGSGGDMGSSKDKMWAAGAGAGEEDVDLELAL
GYKVRSSDMADVAKLEQLQLEAMGMSGVGAGATADDGFVSHLATDTVHNPSSDLSSW
VESMLSELNAPPAPLPAPAPLASTSTSTVSGAAGAGYEDLPAYDSSSTYALK
PIPSVAAPADPSTDSAREPKRMRTGGSTSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
QASAAANGPAVPVYVDTQEGIRLVHALLACAEAVQENFSAEALVKOIPMLASSQ
GGAMRKVAAYFGEALARRVYRFRPPDSSLDAADFADLLHAHFYESCPLKFAHFTAN
QAILEAFAGCRVRVVDGFKOGQMPALLQALALRPGGPPSPFLTGVGPQDETD
LOOVGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGDDTDDEPVIYVNSVFE
LHRLLAOPGALEKVLGTVRVPRIVTVYVEQENHNHNSGTFELDRFTESLHYISTMPSL
EGAGAGSGSTDRAPAAAGTDDQVSEVILGROICNVVACEGARTERTHETIGQWRSR
LGSGFAPVHLGNSNAYKQASTLLALFAGGDDGYRVEBKDGCLTLGWHTRLIATSAWRY
AAAAAP"
BASE COUNT   268 a 684 c 655 g 283 t
ORIGIN
alignment_scores
  Quality:   78.00      Length:   17
  Ratio:     4.588      Gaps:     0
  Percent Similarity: 100.000      Percent Identity: 94.118
alignment_block:
US-09-485-529-104 x ZMA242530      ..
Align seg 1/1 to: ZMA242530 from: 1 to: 1890
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
112 GATGAGCTGCTGGCGGCGCTCGGTACAAAGTGGCGTTCGCGATATGGC 161
17 a 17
|
162 G 162
seq_name: gb_pat:AX005806
seq_documentation_block:
LOCUS      AX005806      2255 bp      DNA      PAT      24-AUG-2000
DEFINITION Sequence 15 from Patent WO9909174.
ACCESSION   AX005806
VERSION     AX005806.1 GI:9928803
KEYWORDS
SOURCE      Zea mays.
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS      Harberd,N.P. and Peng,J.
TITLE        Genetic control of plant growth and development
JOURNAL      Patent: WO 9909174-A 15 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source       Location/Qualifiers
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            /db_xref="taxon:4577"
BASE COUNT   334 a 817 c 737 g 367 t
ORIGIN
alignment_scores
  Quality:   78.00      Length:   17
  Ratio:     4.588      Gaps:     0
  Percent Similarity: 100.000      Percent Identity: 94.118
alignment_block:
US-09-485-529-104 x AX005806      ..
Align seg 1/1 to: AX005806 from: 1 to: 2255
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
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308 GATGAGCTGCTGCGCGCTCGGTACAAGGTGCGTTCGTCGGATATGCG 357

17 a 17

358 G 358

seq_name: gb_pl:AB030956

seq_documentation_block: 2500 bp mRNA PLN 30-MAR-2000
LOCUS AB030956
DEFINITION Oryza sativa mRNA for OsGAI, complete cds.
ACCESSION AB030956
VERSION AB030956.1 GI:6970471
KEYWORDS OsGAI.
SOURCE Oryza sativa (cultivar:Nipponbare) seedling cDNA to mRNA.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (sites)
Ogawa,M., Kusano,T., Katsumi,M. and Sano,H.
Rice gibberellin-insensitive gene homolog, OsGAI, encodes a
nuclear-localized protein capable of gene activation at
transcriptional level
Gene 245 (1), 21-29 (2000)
JOURNAL MEDLINE
REFERENCE 2 (bases 1 to 2500)
Sano,H., Ogawa,M. and Kusano,T.
Direct Submission
TITLE Submitted (09-AUG-1999) to the DDBJ/EMBL/GenBank databases.
Mikihiro Ogawa, Nara Institute of Science and Technology, Plant
Molecular Breeding; Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail:m-ogawa@nsl.nara.ac.jp, Tel:+81-743-72-5652,
Fax:+81-743-72-5659)

FEATURES

source
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/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/dev_stage="seedling"
216..2093
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216..2093
/gene="OsGAI"
/note="GAI homolog"
/codon_start=1
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/protein_id="BAA90749.1"
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LGKYVRSSDMADVAQKLEOLEMAMGCVSAPGAADGCFVSHLATDVTYHNPDLSSW
VESMLSELNAPLPPIPPAPPAARHASTSTVTGGSGGFELPAADSSSTYALRPI
SLPVVATADPSAADSARDTKMRRTGGASTSSSSSSSLGGASRGSVVEAPATQG
AAANAAPVVPVVDTEAGIRLVHALLACAEVQOENFAAAELVKQIPTLAASQGG
AMRVVAYFGALARYVRFPADSTLLDAFADLLHAHFEYSCPYLKFAHFTANQAI
LEAFAGCHRVHVDGFKQGMWPALLQALAPCGPPSPFLTGVPQPDETDALQQ
VGMKLAQFAHTIRYDFOYGLVAAATLADLEPMLQPEEADANEPEVIAVNSVFELH
RLLAQGALEKVLGTVHVRPRITVTVQOENHNHSGSFLDREFTSLHYISTMDSLEG
GSSGQAEISPPAAGGGGTDQVMSEVILGRQICNVACEGNERETHEHETLQWNRNLG
RAGFEPVHLGSNATYKQASTLLALFAGDGYRVEBKGLTGLGWHTRLIATSAWRVAA
A"

BASE COUNT 413 a 861 c 771 g 455 t

alignment_scores:

Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AB030956 ..

Align seg 1/1 to: AB030956 from: 1 to: 2500

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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330 GACGAGCTGCTGCGCGCTCGGTACAAGGTGCGTTCGTCGGACATGCG 379

17 a 17

380 C 380

seq_name: gb_pl:AC087797

seq_documentation_block:
LOCUS AC087797 122497 bp DNA PLN 03-MAY-2001
DEFINITION Oryza sativa chromosome 3 BAC OSJNB0022E02 genomic sequence,
complete sequence.
ACCESSION AC087797
VERSION AC087797.5 GI:13699786
KEYWORDS HTG.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 122497)
Buell,C.R., Yuan,Q., Ouyang,S., Moffat,K.S., Hill,J.N.,
Gansberger,K., Brenner,M., Burgess,S., Hance,M., Shvartsbeyn,M.,
Tsitrin,T., Riggs,F., Hsiao,J., Zismann,V., Blunt,S., Pal,G.,
Vanaken,S.E., Utterback,T.R., Feldblyum,T.V., Quackenbush,J.,
Salzberg,S.L., White,O. and Fraser,C.M.
Oryza sativa chromosome 3 BAC OSJNB0022E02 genomic sequence
Unpublished
2 (bases 1 to 122497)
Buell,R.
Direct Submission
TITLE Submitted (25-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 3 (bases 1 to 122497)
Buell,R.
Direct Submission
TITLE Submitted (20-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
REFERENCE 4 (bases 1 to 122497)
Buell,R.
Direct Submission
TITLE Submitted (03-MAY-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuella@tigr.org
On Apr 20, 2001 this sequence version replaced gi:13605985.
Address all correspondence to:rice@tigr.org
BAC clone OSJNB0022E02 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
clone.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (<http://www.softberry.com/>),
gscan and Genscan (Chris Burge,
<http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky,
<http://genemark.biology.gatech.edu/genemark/>), and Gensplcer
(Mihaela Perlea and Steven Salzberg, contact mperlea@tigr.org).
searches of the complete sequence against a peptide database and
the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shtml>).
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as unknown proteins.
Genes without protein or EST similarity, that are predicted by more
than two gene prediction programs over most of their length are
annotated as hypothetical proteins. Genes encoding tRNAs are
predicted by tRNAscan-SE (Sean Eddy,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are
identified by repeatmasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).
Location/Qualifiers

FEATURES

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source
1. 122497
/organism="Oryza sativa"
/cultivar="Nipponbare"
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complement(1271..1579)
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/note="predicted by fgenesh"
complement(1271..1579)
/gene="OSJNB0022E02.11"
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/protein_id="AAK50135.1"
/db_xref="GI:13937304"
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/db_xref="GI:13937302"
/translation="MRASVFTGVHNSVPLERVQLGATLRPGCGSGARNVGRGSTAA
GSDNTENGEDTNGAFAVFSITAPAPQNTGTGATVREEL"
complement(join(<5240..5517,5605..5684,6132..6212,
6314..6383,6539..6613,6693..6898,7117..7426,7506..7551,
8773..8842,9564..9633,11257..11341,11440..11524,
11608..11698,12255..>12557))
/gene="OSJNB0022E02.2"
complement(5240..12557)
/gene="OSJNB0022E02.2"
/note="EST D47656, AU088605 from this gene"
complement(join(5439..5517,5605..5684,6132..6212,
6314..6383,6539..6613,6693..6898,7117..7426,7506..7551,
8773..8842,9564..9633,11257..11341,11440..11524,
11608..11698,12255..12388))
/gene="OSJNB0022E02.2"
/codon_start=1
/product="unknown protein"
/protein_id="AAK50136.1"
/db_xref="GI:13937305"
/translation="MQRRAQTWAGVKTAQAAAAHAALFCFTLLIALKVKDGTAYSW
WIIFLWLFHGVGRFSMPAPSLPHGRHWAPCHSIVAAPLLIAELLCIYLES
RVKSTVDATKIVFLPPLAEVILADNFRMCALMPGDESMDEAIWETLPHFWA
ISNVFTIATFTLLKSGDVAGLWDLFINYGIAECFAFLVCTRWENPMHKSNP
GEASSSAIRVDWESGLLPSELDHEQERLCGLPDIGSHVNMKIPLVIFQVLLCML
ETAPPAAQIPIPALFSPILFQAGVILFSLARLEKVLRLNRNGVSPNLTISKV
RDCFAFLRGLLGMWSIDEGSKEQARLFYTESTGYNTFCGPEVVRKMPKRDLA
EEVRLQAALGESEITKCTKQFERLQNEKVLRCRYEGEICMVLPLPCRHTLKTC
SDKKCKPCICRVPIEERMPVDV"
complement(12328..12420)
/product="hypothetical protein"
/rpt_family="CGGGG"
/rpt_family="(GA)n"
join(<14168..15023,15131..15274,15344..16687,16818..17803,
17887..18048,18262..>18366)
/gene="OSJNB0022E02.12"
14168..18366
/note="OSJNB0022E02.12"
/note="similar to gag pol polyprotein GB:AAD12997
GI:4234852 (Zea mays)"
join(14168..15023,15131..15274,15344..16687,16818..17803,
17887..18048,18262..>18366)

repeat_region
/product="hypothetical protein"
/protein_id="AAK50123.1"
/db_xref="GI:13937292"
/translation="MAAGSGARAVGNGGGVGGGPPAPASLPPLPRHPSPRRRTPA
SPGLJLPTLRQYSTGSLPESAAGHAYATPRSPRRGADADEGEVLGLSSAAV
WMGAQARSCEGNAESMAVALSACPYAGDIALAKGEATHGCGVMKGVIHGVIYFTISL
VCVMGKLGEMDNAAKAFRADATEKNIVTWNTLITSYATAGLCEALDVLQAQMEIQGTV

alignment_scores:
Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

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17887..18048,18262..18366)
/gene="OSJNB0022E02.12"
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/protein_id="AAK50117.1"
/db_xref="GI:13937286"
/translation="MAGFADALPRDKFTGVHFKRWQIRVTLMLTAMKCFWVSTGKPEG
VLTAEQOKFEATTLFVGCILSVGLDRIVEVYMHMTDAKELWDALNTKFGATDASND
FYTALMKRQEYSVEGLIASLDEVERAREKDAASKGDSOSANVHVHQAQNSKGYK
LCTALHKKQEYSGEGLIASLDEVERAREKDAASKGDSOSANVHVHQAQNSKGYK
AQOTTFKQKNNPNQDERTCFVCGQVGHARAKCPQPKQKMAAGTQSKSANVTI
GNTDGGSGYRTGFRHPNGEWITCFSCWCHGRSEVIFGKDRAAEERAAACPFTRQESC
YEGGLFRFSLDFCQPKPHKAAERNLAPLELLHSDLCMEMGVLTKGKRYFTMLID
DATRFVYLLTKTDEALDYFKIYKAEVENOLDKIKRLRSDRGGEFFSNEFDLCEE
IVKGSCHSCVQKQKPKHAAERNLAPLELLHSDLCMEMGVLTKGKRYFTMLID
HGIIHRTPYSPESNGIAERKNRTITDLVNAMLDTAGLPKAWMGALLTSHVLNRV
PNRNDKTPYEIHWGRKPSLSYLRWTGCLAKVNPITKKRKLGPKTVDVCLGYAHS
IAYRLIVSEVPMHVGTIMESRDATFFESFFPMKDTSHSGSQSEIIPSSITPPEQ
TEHTHELVEEDSEAPRRSKRQRTAKSGDDFTVYLVDDTPKSISEAYSPADYWK
EAVRSEMDSTIANGTWERTPYGCKPVGCKWFKKLRDPADSHGLLVHOMDYKTAFL
NGELDEIYMDQDPGVFVGEQGVCKLLKSLYGLKQAQKQHEKFDKTLTSAGFAVN
EADKVVYRHGGEGVILCYVDIILFIGNLEVINEVKSFLSONDKDLGVADVIL
NIKLIRGNGITLLOSHYVEKILNRECYIDSKPSPTPYDPSLLLRKNKRIARNOLEYS
QIIGSLMYLSATRPDISFAVSKLSRFTSNPGDDHWRALERVMRYLKGTVELGLHTG
YPALLEGYSDSNWISDVDEIKATSGYVFTLGGGAVSWRSCKQTILTRTMEAEULTAD
TATVAEWLRDLMLDPVVEKPTCEKTIIEVCQIKKILRSYNVGLHPNSEKPGRSLHEG
TITKCDRQCTEGDGFETHSILEGTCIELDCWQSQMKILGESSRKLTLDLGV"
complement(18822..18858)
/rpt_family="(CAGGC)n"
complement(19612..19640)
/rpt_family="AT_rich"
complement(20459..20487)
/rpt_family="AT_rich"
<21271..>21576
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21271..21576
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/note="predicted by fgenesh"
21271..21576
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/codon_start=1
/product="hypothetical protein"
/protein_id="AAK50120.1"
/db_xref="GI:13937289"
/translation="MTTRTVLLSEYSDSGHDSGRNGAVAGVVGHVGGAGGRLHGYI
ACAVILLASPYAPLHIQDELQHWYATKDCRWQAPAWDVEDYEPTSNDASVPNS"
complement(22507..22529)
/rpt_family="(TA)n"
complement(22544..22588)
/rpt_family="AT_rich"
complement(23124..23217)
/rpt_family="(GGAGAA)n"
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complement(23165..25551)
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/gene="OSJNB0022E02.14"
/codon_start=1
/product="hypothetical protein"
/protein_id="AAK50123.1"
/db_xref="GI:13937292"
/translation="MAAGSGARAVGNGGGVGGGPPAPASLPPLPRHPSPRRRTPA
SPGLJLPTLRQYSTGSLPESAAGHAYATPRSPRRGADADEGEVLGLSSAAV
WMGAQARSCEGNAESMAVALSACPYAGDIALAKGEATHGCGVMKGVIHGVIYFTISL
VCVMGKLGEMDNAAKAFRADATEKNIVTWNTLITSYATAGLCEALDVLQAQMEIQGTV

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alignment_block:
US-09-485-529-104 x AC087797 ..
Align seg 1/1 to: AC087797 from: 1 to: 12497

1 Asp6LeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
|||||
69197 GAGCAGCTGTCGGCGCGTCGGGTACAGGTGCGGTCCGACATGGC 69246
17 a 17
1
69247 C 69247

seq_name: gb_pat:AX005810

seq_documentation_block:
LOCUS AX005810 725 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 19 from Patent WO9909174.
ACCESSION AX005810
VERSION AX005810.1 GI:9928807
KEYWORDS
SOURCE
ORGANISM
Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 725)
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 19 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source
1..725
/organism="Oryza sativa"
/db_xref="taxon:4530"
misc_feature
171 /note="n is any nucleotide"
misc_feature
302 /note="n is any nucleotide"
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427 /note="n is any nucleotide"
misc_feature
444 /note="n is any nucleotide"
misc_feature
459 /note="n is any nucleotide"
misc_feature
711 /note="n is any nucleotide"
BASE COUNT 98 a 226 c 276 g 119 t 6 others
ORIGIN

alignment_scores:
Quality: 72.00 Length: 16
Ratio: 4.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 93.750

alignment_block:
US-09-485-529-104 x AX005810 ..
Align seg 1/1 to: AX005810 from: 1 to: 725

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
|||||
109 GAGCTGTCGGCGCGTCGGGTACAGGTGCGGTCCGACATGGCC 156

seq_name: gb_pat:AX005867

seq_documentation_block:
LOCUS AX005867 324 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 76 from Patent WO9909174.
ACCESSION AX005867
VERSION AX005867.1 GI:9928862
KEYWORDS

SOURCE
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 324)
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 76 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES
source
1..324
/organism="Triticum aestivum"
/db_xref="taxon:4565"
misc_feature
158 /note="n is any nucleotide"
misc_feature
161 /note="n is any nucleotide"
misc_feature
217 /note="n is any nucleotide"
BASE COUNT 39 a 141 c 85 g 56 t 3 others
ORIGIN

alignment_scores:
Quality: 70.00 Length: 15
Ratio: 4.667 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-485-529-104 x AX005867/rev ..
Align seg 1/1 to reverse of: AX005867 from: 1 to: 324

3 LeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
|||||
156 CTGCTGGCGCGCTCGGTACAGGTGCGCGCTCCGACATGGCG 112

seq_name: gb_pl:ATRG2

seq_documentation_block:
LOCUS ATRG2 1951 bp mRNA PLN 19-AUG-1997
DEFINITION A.thaliana mRNA for RGA2 gene.
ACCESSION Y11337
VERSION Y11337.1 GI:2339979
KEYWORDS RGA2 gene.
SOURCE thale.cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1 (bases 1 to 1951)
AUTHORS Truong,H.N., Caboche,M. and Daniel-Vedele,F.
TITLE Sequence and characterization of two Arabidopsis thaliana cDNAs
isolated by functional complementation of a yeast gln3 gdh1 mutant
JOURNAL FEBS Lett. 410 (2-3), 213-218 (1997)
MEDLINE 97379310
REFERENCE
2 (bases 1 to 1951)
AUTHORS Truong,H.N.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
FEATURES
source
1..1951
/organism="Arabidopsis thaliana"
/sub_species="L). Heynh"
/db_xref="taxon:3702"
/dev_stages="two-leaf stage seedlings"
/note="Landsberg erecta ecotype"
196..1794
/gene="RGA2"
196..1794
CDS
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/ gene="RGA2"
/ codon_start=1
/ product="RGA2 protein"
/ protein_id="CAA72178.1"
/ db_xref="GI:2339980"
/ db_xref="SPTREMBL:O23643"
/ translation="MKRDHHHHQDKKTKMMNEEDGNGMDELLAVLGVKVRSEMA
VAQKLEQVMSNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLK
AIPGDAILNQFAIDSASSNQGGDTYTNKRLKCSNGVVTETTTAESTRHVVLVD
SOENGVRLVHALLACAEVOKENLTVAEALVKQIGFLAVSQIGAMRVATYFAEALAR
RIVRLSPSPIDHSLSDTLQMHFYETCPYLKFAHFTANOAILLEAFQGKKRVVIDFS
MSQGLQWPAALMALRPGPPVFRLTGIGPPAPDNFDYLHEVGCCKLAHLAEAHVEF
EYRGFVANTLADLADLMLELRSEISVAVNSVFEHLKLGRLPGADIKVLGVVNOIKP
EFTVVEQESNHNPIFLDRFTESLHYITLFDSEGVPSGQDKVMSEVYLGKQICNV
VACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEES
DGCLMLGWHTRPLIATSAWKLSTN"

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BASE COUNT 482 a 419 c 475 g 575 t
ORIGIN

alignment_scores:
Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x ATRGA2

Align seg 1/1 to: ATRGA2 from: 1 to: 1951

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1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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274 GATGAGCTCTCAGCTGTTCTGGTTACAGGTTAGTTCATCGGAATGCG 323

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17 a 17

324 T 324

seq_name: gb_pat:A64697

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seq_documentation_block:
LOCUS A64697 1964 bp DNA PAT 29-MAR-1999
DEFINITION Sequence 1 from Patent WO9729123.
ACCESSION A64697
VERSION A64697.1 GI:4530762
KEYWORDS
SOURCE thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1964)
Harberd,N.P., Peng,J., Carol,P. and Richards,D.E.
NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA
Patent: WO 9729123-A 1 14-AUG-1997;
INNES JOHN CENTRE INNOV LTD (GB)
Other publication AU 1799697 19970828.
COMMENT Location/Qualifiers
FEATURES
source
1..1964
/organism="Arabidopsis thaliana"
/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
/chromosome="1"
/map="20.9"
/haplotype="GAI"

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BASE COUNT 489 a 426 c 474 g 575 t
ORIGIN

alignment_scores:
Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x A64697

Align seg 1/1 to: A64697 from: 1 to: 1964

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1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
287 GATGAGCTCTCAGCTGTTCTGGTTACAGGTTAGTTCATCGGAATGCG 336

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17 a 17

337 T 337

seq_name: gb_pl:ATY15193

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seq_documentation_block:
LOCUS ATY15193 1964 bp DNA PLN 01-NOV-1997
DEFINITION Arabidopsis thaliana GAI gene.
ACCESSION Y15193
VERSION Y15193.1 GI:2569937
KEYWORDS GAI gene.
SOURCE thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1964)
Peng,J., Carol,P., Richards,D.E., King,K.E., Cowling,R.J.,
Murphy,G.P. and Harberd,N.P.
The Arabidopsis GAI gene defines a signalling pathway that
negatively regulates gibberellin responses
Genes Dev. In press
2 (bases 1 to 1964)
Harberd,N.P.
Direct Submission
Submitted (22-OCT-1997) N.P. Harberd, John Innes Centre, Molecular
Genetics, Colney Lane, Norwich, NR4 7UJ, UK
Location/Qualifiers
1..1964
/organism="Arabidopsis thaliana"
/strain="Landsberg erecta"
/db_xref="taxon:3702"
/chromosome="1"

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gene

CDS

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209..1807
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/ gene="GAI"
/ codon_start=1
/ protein_id="CAA75492.1"
/ db_xref="GI:2569938"
/ db_xref="SPTREMBL:O23724"
/ translation="MKRDHHHHQDKKTKMMNEEDGNGMDELLAVLGVKVRSEMA
VAQKLEQVMSNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLK
AIPGDAILNQFAIDSASSNQGGDTYTNKRLKCSNGVVTETTTAESTRHVVLVD
SOENGVRLVHALLACAEVOKENLTVAEALVKQIGFLAVSQIGAMRVATYFAEALAR
RIVRLSPSPIDHSLSDTLQMHFYETCPYLKFAHFTANOAILLEAFQGKKRVVIDFS
MSQGLQWPAALMALRPGPPVFRLTGIGPPAPDNFDYLHEVGCCKLAHLAEAHVEF
EYRGFVANTLADLADLMLELRSEISVAVNSVFEHLKLGRLPGADIKVLGVVNOIKP
EFTVVEQESNHNPIFLDRFTESLHYITLFDSEGVPSGQDKVMSEVYLGKQICNV
VACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEES
DGCLMLGWHTRPLIATSAWKLSTN"

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BASE COUNT 489 a 426 c 474 g 575 t
ORIGIN

alignment_scores:

Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x ATY15193

Align seg 1/1 to: ATY15193 from: 1 to: 1964

1 AspCluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 287 GATGAGCTTCGCTGTTCTGTTAGTTACAAAGTTAGGTCATCGGAATGGC 336

17 a 17
 337 T 337

seq_name: gb_pl.ATY15194

seq_documentation_block: 2201 bp mRNA PLN 01-NOV-1997
 LOCUS ATY15194
 DEFINITION Arabidopsis thaliana mRNA for GRS protein.
 ACCESSION Y15194
 VERSION Y15194.1 GI:2569939
 KEYWORDS GRS protein.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 2201)
 AUTHORS Peng, J., Carol, P., Richards, D.E., King, K.E., Cowling, R.J.,
 Murphy, G.P., and Harberd, N.P.

TITLE The Arabidopsis GAI gene defines a signalling pathway that

negatively regulates gibberellin responses

Genes Dev. In press

REFERENCE 2 (bases 1 to 2201)

AUTHORS Harberd, N.P.

TITLE Direct Submission

JOURNAL Submitted (22-OCT-1997) N.P. Harberd, John Innes Centre, Molecular

Genetics, Colney Lane, Norwich, NR4 7UJ, UK

FEATURES Location/Qualifiers

1..2201

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/chromosome="2"

144..1907

/codon_start=1

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/protein_id="CAA75493.1"

/db_xref="GI:2569940"

/db_xref="SPTREMBL:O23725"

/translation="MKRDHGFQGRLSNHGTSSTSSSSSKDKMMVKKEEDGGNMD
 ELLAVLYKVRSEMAEVALKEOLETMMSNVQEDGLSHLAADTVHYNPSELYSWLND
 MLSELNPPPLPASSNGLDPLVPSPEICGFPSADYDLVPGNAIQFPAIDSSSSNN
 QNRLKSCSPDSMVTSTGTQIGGVIGTITVTITTTTAAESTRVSAILVDSQENG
 VRLVHALMACAEAIQNNLTAEALVKQIGCLAVSQACAMRKVATYFAEALARIYRL
 SPQNIQDHLSDTLQMHFTETCYLKFAHFTANOAILAEAFEGKRVHVIDFSMNQGL
 QMPALQALALREGGPPFTFRLTGIGPPAPDSDHLHEYGCKLAOLAEAHVFEFFYRGF
 VANSIADLMSLELRPSDTEAVNSVFELHKLGRPGGIEKVLGVVVKQIKPVITV
 VEQSNHNGPVLDRFTESLHYSTLFDLSLEGVPNSODKVMSEVYLGKQICNLVACEG
 PDRVERHETLSQWGNRFSGSLAPAHLSNAFAKQASMLLSVFNSSQGYRVEESNGCLM
 LGWHTPLTITSNAWKLSTAA"

BASE COUNT 576 a 450 c 525 g 650 t
 ORIGIN

alignment_scores:

Quality: 70.00 Length: 17
 Ratio: 4.118 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x ATY15194

Align seg 1/1 to: ATY15194 from: 1 to: 2201

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 273 GATGAGCTTCGCTGTTCTGTTAGTTACAAAGTTAGGTCATCGGAGATGGC 322

17 a 17
 323 G 323

seq_name: gb_pl.ATRGAL

seq_documentation_block: 2210 bp mRNA PLN 19-AUG-1997
 LOCUS ATRGAL
 DEFINITION A.thaliana mRNA for RGAL gene.
 ACCESSION Y11336
 VERSION Y11336.1 GI:2339977
 KEYWORDS RGAL gene.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 2210)

AUTHORS Truong, H.N., Caboche, M. and Daniel-Vedele, F.

TITLE Sequence and characterization of two Arabidopsis thaliana cDNAs
 isolated by functional complementation of a yeast gln3 gdh1 mutant

JOURNAL FEBS Lett. 410 (2-3), 213-218 (1997)

MEDLINE 97379310

REFERENCE 2 (bases 1 to 2210)

AUTHORS Truong, H.N.

TITLE Direct Submission

JOURNAL Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
 de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
 FRANCE

FEATURES Location/Qualifiers

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/organism="Arabidopsis thaliana"

/sub_species="(L). Heynh"

/db_xref="taxon:3702"

/dev_stage="two-leaf stage seedlings"

/note="Landsberg erecta ecotype"

132..1895

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132..1895

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/codon_start=1

/product="RGAL protein"

/protein_id="CAA72177.1"

/db_xref="GI:2339978"

/translation="SPTREMBL:O23642"

/translation="MKRDHGFQGRLSNHGTSSTSSSSSKDKMMVKKEEDGGNMD
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 MLSELNPPPLPASSNGLDPLVPSPEICGFPSADYDLVPGNAIQFPAIDSSSSNN
 QNRLKSCSPDSMVTSTGTQIGGVIGTITVTITTTTAAESTRVSAILVDSQENG
 VRLVHALMACAEAIQNNLTAEALVKQIGCLAVSQACAMRKVATYFAEALARIYRL
 SPQNIQDHLSDTLQMHFTETCYLKFAHFTANOAILAEAFEGKRVHVIDFSMNQGL
 QMPALQALALREGGPPFTFRLTGIGPPAPDSDHLHEYGCKLAOLAEAHVFEFFYRGF
 VANSIADLMSLELRPSDTEAVNSVFELHKLGRPGGIEKVLGVVVKQIKPVITV
 VEQSNHNGPVLDRFTESLHYSTLFDLSLEGVPNSODKVMSEVYLGKQICNLVACEG
 PDRVERHETLSQWGNRFSGSLAPAHLSNAFAKQASMLLSVFNSSQGYRVEESNGCLM
 LGWHTPLTITSNAWKLSTAAH"

BASE COUNT 583 a 454 c 518 g 655 t
 ORIGIN

alignment_scores:

Quality: 70.00 Length: 17
 Ratio: 4.118 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x ATRGAL

Align seg 1/1 to: ATRGAL from: 1 to: 2210

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1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
261 GACGAGCTTCGCGTGTAGTTACAAAGTTAGTTCATCGGAGATGCG 310

17 a 17
|
311 G 311

seq_name: gb_pl:ATA224957

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DEFINITION   Arabidopsis thaliana RGAL gene.
ACCESSION   AJ224957
VERSION     AJ224957.1 GI:3021335
KEYWORDS    RGAL gene.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 4081)
Sanchez-Fernandez.R., Ardiles-Diaz.W., Van Montagu.M., Inze,D. and
May,M.J.
Cloning of the Arabidopsis thaliana RGA-like gene, a putative
member of the VHIID domain transcription factor family
Unpublished
2 (bases 1 to 4081)
Sanchez-Fernandez.R.
Direct Submission
Submitted (14-MAR-1998) Sanchez-Fernandez R., Department of
Genetics, University of Gent (VIB), K.L. Ledeganckstraat 35, 9000
Gent, BELGIUM

FEATURES             Location/Qualifiers
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1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
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1968 GACGAGCTTTGGTGTGTTAGTTACAAAGTTGATCATCGGACATGCG 2017

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2018 T 2018

seq_name: gb_pl:ATK3M16

seq_documentation_block:
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DEFINITION   Arabidopsis thaliana DNA chromosome 5, BAC clone K3M16 (ESSA
project).
ACCESSION   AL391150
VERSION     AL391150.1 GI:9755767
KEYWORDS    thale cress.
SOURCE      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 24604)
Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asanizu,E., Kotani,H.,
Tabata,S., Mewes,H.W., Rudd,S., Lemcke,K. and Mayer,K.F.X.
Unpublished
2 (bases 1 to 24604)
EU Arabidopsis sequencing,project.
Direct Submission
Submitted (07-AUG-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
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TPDQLEDEYGSFLENIVKDFREYADVFTTEYGGVKKNWITFNEPWFVAHAGYDVCKK
APGRCSRYLKGCEDRGSRGYEAYLYSHNLLNHAHAENEVFRQKYGGKIGIAHSPAW
FEPHDUKSDNDVPTVSXVLDFMLGWHLDPTFGDIYPOIMKDLGLHRLPKFTSSOKAKL
KSTDFVGLNYITSTFNHNEKPPDPTSPKQDSLVAWEKPNVDHSAIGSQPLTAALP
VYAKGFRSLKYIKDYANPEIMMENGYGDKLKDSDSEVGADYNRKYYLQRLHLLA
MNEAICIDKRVTVGYFVWSLLDNFEWQDGYNNRFGLYYVDFKNNLTRYEKESAKYYKD
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  Percent Similarity: 100.000  Percent Identity: 82.353

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50117 T 50117

seq_name: gb_pl:AC005560

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LOCUS AC005560 95137 bp DNA PLN 05-APR-2000
DEFINITION Arabidopsis thaliana chromosome II section 3 of 255 of the complete
sequence. Sequence from clones F10A8, F219.
ACCESSION AC005560 AE002093
VERSION AC005560.2 GI:6598472
KEYWORDS HTG.
SOURCE
ORGANISM Arabidopsis thaliana

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Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 95137)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
Fuji,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Renning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Unayam,L.,
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
Venter,J.C.

```

Sequence and analysis of chromosome 2 of the plant Arabidopsis

thaliana

Nature 402 (6763), 761-768 (1999)

JOURNAL MEDLINE

20083487

PUBMED 10617197

REFERENCE 2 (bases 1 to 95137)

AUTHORS Lin,X.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

COMMENT

On Dec 17, 1999 this sequence version replaced gi:3785968. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (<http://www.tigr.org/tdb/at/at.html>).

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (<ftp://arthur.epm.ornl.gov/pub/xgrail>), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, <http://gnomc.stanford.edu/GENSCANW.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetGene2/>), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats were identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

FEATURES	Location/Qualifiers
source	1..95137 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db_xref="taxon:3702" /chromosome="II"
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CDS	/note="F219.1; predicted by genscan" 341..997 /gene="At2g01390" /note="hypothetical protein" /codon_start=1 /protein_id="AAC67316.1" /db_xref="GI:3785969"
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mRNA	complement(1085..1127) /rpt_family="(TAAAA)n" join(<1175..1294,1620..>1940) /gene="At2g01400"
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Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

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seq_name: gb_pl:AC006917

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LOCUS AC006917 132599 bp DNA PLN 28-JUN-2000
DEFINITION Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
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ACCESSION AC006917
VERSION AC006917.6 GI:4757662
KEYWORDS HTG.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 132699)
Chao,Q., Shinn,P., Dunn,P., Buehler,E., Kahn,S., Kim,C., Walker,M.,
Williams,S., Altafi,H., Araujo,R., Conn,L., Conway,A.B.,
Gonzalez,A., Hansen,N.F., Huizar,L., Kremenetskaia,I., Lenz,C.,
Li,J., Liu,S., Luros,S., Rowley,D., Schwartz,J., Toriumi,M.,
Vysocha,V., Yu,G., Davis,R.W., Federspiel,N.A., Theologis,A. and
Ecker,J.R.
Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
I
Unpublished
2 (bases 1 to 132699)
Ecker,J.R.
Direct Submission
Submitted (25-FEB-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
```

REFERENCE AUTHORS TITLE JOURNAL	3 (bases 1 to 132699) Ecker,J.R. Direct Submission Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	CDS	GIAGKSKAEFOAPCRRTKYPREIPLPWYRSALPQMAGFLPFPFSAIYELIYVIFAS VWGHRIYIISILFIVFIIITVAFITVATVYFQALAEEDHOMWRSFLCGSGTGLFI YAYCLYYIYARSOMSGFMQTSFFSGYMACICYGFFLMLGTGVGFRAALLFVRHYRSIK CE"
REFERENCE AUTHORS	4 (bases 1 to 132699) Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bel,B., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J. Direct Submission Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On May 7, 1999 this sequence version replaced gi:4731042. Location/Qualifiers 1. 132699 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" complement(join(144..278,360..491,576..673,814..1435, 1749..1867,2161..2310,2441..2565,2698..2742,2837..2902, 2979..3031,3117..3234,3314..3415,3498..3655,3741..3818, 3894..3985,4054..4104,4138..4420)) /note="similar to Na/H antiporter dbj BAA89487.1" /codon_start=1 /evidence=not_experimental /product="F10B6.1" /protein_id="AAF79251.1" /db_xref="GI:8778242"	CDS	8842..9714 /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F10B6.4" /protein_id="AAF79218.1" /db_xref="GI:8778209" /translation="MDLSREVDFOPIKETIDHSGLPLSDVLMQKLKLTAEESQRRLRE QYLSLVRLKEKEKVIDLVRSEASMAQSLKKFVEENQKLGSEDEDLVNQCCKWEKEC FLYHQDRESLMFENETDERAREAESEVRELEERKMSDEIKRSIESEDLVDLSIL ASFVQSDSISLGRIFLEANSEDKCCTELLRKWDOLKPTTKQFVSLVSMVKRIEKEK ECLIMNLAKAEQVELVSEQNRELDRENRKFLQCSAERSHSGSKFNKRKSIKMMSSP IEKRIELSSQEEFD" 11067..11906 /note="unknown protein; similar to EST gb AI995472.1" /codon_start=1 /evidence=not_experimental /product="F10B6.5" /protein_id="AAF79219.1" /db_xref="GI:8778210" /translation="MDDDGFRNMGYYEPAAATFGNGLQMLMSTIDNTKTPFLPGRDP NLMGPNQSYHHQEPPIHMSYNWQKDKFNNMLPYTTATPNYGNVLPETSSAPSHQ MNLHHQLQTEENPVKLEETIVVOTKKRKTNAKAGSTPAKKPRKPKDENSENNNNNT NVTRVKPAKSDVLIVNGVSMDSGLPVPICCTGAPQCYRMCGGQWQACCTTNTS MHPLPMSKTRRGARISGRKMSQGAFFKVKLEKLASDGFNPGNPIDLKSHWARHGNTKFV TIR"
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REFERENCE AUTHORS TITLE JOURNAL	3 (bases 1 to 132699) Ecker,J.R. Direct Submission Submitted (07-MAY-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	CDS	GIAGKSKAEFOAPCRRTKYPREIPLPWYRSALPQMAGFLPFPFSAIYELIYVIFAS VWGHRIYIISILFIVFIIITVAFITVATVYFQALAEEDHOMWRSFLCGSGTGLFI YAYCLYYIYARSOMSGFMQTSFFSGYMACICYGFFLMLGTGVGFRAALLFVRHYRSIK CE"
REFERENCE AUTHORS	4 (bases 1 to 132699) Cheuk,R., Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bel,B., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J. Direct Submission Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA On May 7, 1999 this sequence version replaced gi:4731042. Location/Qualifiers 1. 132699 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" complement(join(144..278,360..491,576..673,814..1435, 1749..1867,2161..2310,2441..2565,2698..2742,2837..2902, 2979..3031,3117..3234,3314..3415,3498..3655,3741..3818, 3894..3985,4054..4104,4138..4420)) /note="similar to Na/H antiporter dbj BAA89487.1" /codon_start=1 /evidence=not_experimental /product="F10B6.1" /protein_id="AAF79251.1" /db_xref="GI:8778242"	CDS	8842..9714 /note="hypothetical protein" /codon_start=1 /evidence=not_experimental /product="F10B6.4" /protein_id="AAF79218.1" /db_xref="GI:8778209" /translation="MDLSREVDFOPIKETIDHSGLPLSDVLMQKLKLTAEESQRRLRE QYLSLVRLKEKEKVIDLVRSEASMAQSLKKFVEENQKLGSEDEDLVNQCCKWEKEC FLYHQDRESLMFENETDERAREAESEVRELEERKMSDEIKRSIESEDLVDLSIL ASFVQSDSISLGRIFLEANSEDKCCTELLRKWDOLKPTTKQFVSLVSMVKRIEKEK ECLIMNLAKAEQVELVSEQNRELDRENRKFLQCSAERSHSGSKFNKRKSIKMMSSP IEKRIELSSQEEFD" 11067..11906 /note="unknown protein; similar to EST gb AI995472.1" /codon_start=1 /evidence=not_experimental /product="F10B6.5" /protein_id="AAF79219.1" /db_xref="GI:8778210" /translation="MDDDGFRNMGYYEPAAATFGNGLQMLMSTIDNTKTPFLPGRDP NLMGPNQSYHHQEPPIHMSYNWQKDKFNNMLPYTTATPNYGNVLPETSSAPSHQ MNLHHQLQTEENPVKLEETIVVOTKKRKTNAKAGSTPAKKPRKPKDENSENNNNNT NVTRVKPAKSDVLIVNGVSMDSGLPVPICCTGAPQCYRMCGGQWQACCTTNTS MHPLPMSKTRRGARISGRKMSQGAFFKVKLEKLASDGFNPGNPIDLKSHWARHGNTKFV TIR"
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ACCESSION AC015886
VERSION AC015886.4 GI:13959257
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 188716)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome, clone CT7-378P20
Unpublished
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
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Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
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Peterson,K., Pollara,V., Riley,K., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wymann,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 7, 2001 this sequence version replaced gi:7230250.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L737
Center clone name: 378_P20
----- Summary Statistics
Sequencing vector: M13; M77815; 82% of reads

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FEATURES

source

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Sequencing vector: Plasmid; n/a; 18% of reads
Chemistry: Dye-primer-amerham; 84% of reads
Chemistry: Dye-terminator Big Dye; 16% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175387 bases at least Q40
Consensus quality: 181747 bases at least Q30
Consensus quality: 184307 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 186216; sum-of-contigs
Quality coverage: 4.8 in Q20 bases.
NOTE: This is a 'working draft' sequence. It currently
consists of 26 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence.
as soon as it is available and the accession number will
be preserved.

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AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 125021)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
TITLE	Direct Submision				
JOURNAL	Submitted (06-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA				
REFERENCE	3 (bases 1 to 125021)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
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JOURNAL	Submitted (08-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA				
REFERENCE	4 (bases 1 to 125021)				
AUTHORS	Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Araujo,R., Huizar,L., Rowley,D., Buehler,E., Dunn,P., Gonzalez,A., Kremenetskaia,I., Kim,C., Lenz,C., Li,J., Liu,S., Luros,S., Schwartz,J., Shinn,P., Toriumi,M., Vyotskaia,V., Walker,M., Yu.G., Ecker,J., Theologis,A. and Davis,R.W.				
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COMMENT	On Jul 9, 1999 this sequence version replaced gi:5019265. e-mail for correspondence: arab@sequence.stanford.edu Genes with similarity to proteins in the databases are described as 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene prediction software are described as 'hypothetical proteins'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge, http://genomic.stanford.edu/~chris/GENSCANW.html), Fexa (V.Solovyev & A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/), NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/NetPlantGene.html) and eMotif(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L., http://motif.stanford.edu/projects.html). Location/Qualifiers 1. .125021 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="I" /map="ni208" /clone="F13F21" complement(4079. .5020)				
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LOCUS AX005855 309 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 64 from Patent WO9909174.
ACCESSION AX005855
VERSION AX005855.1 GI:9928850
KEYWORDS bread wheat.
SOURCE
ORGANISM Triticum aestivum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 309)
AUTHORS Harberd,N.P. and Peng,J.
TITLE Genetic control of plant growth and development
JOURNAL Patent: WO 9909174-A 64 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

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Location/Qualifiers
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ORIGIN

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Percent Similarity: 100.000 Percent Identity: 100.000

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Align seg 1/1 to: AX005855 from: 1 to: 309

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LOCUS RPXX02 312430 bp DNA BCT 12-NOV-1998
DEFINITION Rickettsia prowazekii strain Madrid E, complete genome; segment 2/4.

ACCESSION AJ235271 AJ235269
VERSION AJ235271.1 GI:3868717
KEYWORDS complete genome.
SOURCE Rickettsia prowazekii.
ORGANISM Rickettsia prowazekii.

REFERENCE 1 (bases 1 to 312430)
AUTHORS Rickettsiaceae; Rickettsia; typhus group.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsia; typhus group.
1 (bases 1 to 312430)
Andersson,S.G., Zomorodipour,A., Andersson,J.O.,
Sicheritz-Ponten,T., Alsmark,O.C., Podowski,R.M., Naslund,A.K.,
Eriksson,A.S., Winkler,H.H. and Kurland,C.G.

TITLE The genome sequence of Rickettsia prowazekii and the origin of mitochondria
JOURNAL Nature 396 (6707), 133-140 (1998)
MEDLINE 99039499
REFERENCE 2 (bases 1 to 312430)
AUTHORS Andersson,S.G.E.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S-751 24, SWEDEN
On Nov 13, 1998 this sequence version replaced gi:3860788.

COMMENT
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Estimated insert size: 140602; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.8x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
      (see http://www.ngsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 64 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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ACCESSION  AC020887
VERSION    AC020887.2  GI:7340304
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 271519)
AUTHORS   DOE Joint Genome Institute.
TITLE     Sequencing of Mouse
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 271519)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            On Mar 29, 2000 this sequence version replaced gi:6686421.
COMMENT   -----Genome Center
            Center: Joint Genome Institute
            Center Code: JGI
            Web site: http://www.jgi.doe.gov
            -----Summary Statistics
            Consensus quality: 168487 bases at least Q40
            Consensus quality: 217951 bases at least Q30
            Consensus quality: 233703 bases at least Q20
            Estimated insert size: 271519; sum-of-ctigs estimation
            Estimated insert size: 205000; pulse field gel estimation
            Quality coverage: 3.76x in Q20 bases; pulse field gel estimation
            Quality coverage: 2.84x in Q20 bases; sum-of-ctigs estimation
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 86 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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TITLE CHST1 and CHST2 sulfotransferases expressed by human vascular endothelial cells: cDNA cloning, expression, and chromosomal localization
JOURNAL Genomics 55 (3), 345-347 (1999)
MEDLINE 99168906
REFERENCE 2 (bases 1 to 1241)
AUTHORS Li.X. and Tedder,T.F.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1998) Immunology, Duke University Medical Center, Durham, NC 27710, USA
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SOURCE Homo sapiens
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REFERENCE
AUTHORS Fukuda,M. and Hanebuchi,N.
TITLE KERATAN SULFATE 6-SULFOTRANSFERASE AND DNA CODING FOR THE SAME
JOURNAL Patent: JP 1998155488-A 1 16-JUN-1998; SEIKAGAKU KOGYO CO LTD
COMMENT
OS Homo sapiens (human)
PN JP 1998155488-A/1
PD 16-JUN-1998
PF 29-NOV-1996 JP 1996320535
PI FUKUDA MASAKAZU, HANEBUCHI NAGAMOTO
PC C12N15/09,C07H21/04,C07K14/47,C08B37/00,C12N9/10, PC C12P19/26/C12P21/02,

PC (C12N15/09,C12R1:91),(C12N9/10,C12R1:19);
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CC hypothetical: No;
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ORGANISM Bacillus subtilis
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
REFERENCE
1 (bases 1 to 2096)
AUTHORS Marasco,R., Varcamonti,M., Ricca,E. and Sacco,M.
TITLE A new Bacillus subtilis gene with homology to Escherichia coli prc
JOURNAL Gene 183 (1-2), 149-152 (1996)
MEDLINE 97149292
REFERENCE 2 (bases 1 to 2096)
AUTHORS Sacco,M.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-1996) M. Sacco, Istituto Internazionale di Genetica e Biofisica, via Marconi 10, 80125, Napoli ITALY
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DEFINITION Porcine reproductive and respiratory syndrome virus RNA-dependent
RNA polymerase gene, partial cds.
ACCESSION AF298771
VERSION AF298771.1 GI:10719655
KEYWORDS
SOURCE Porcine reproductive and respiratory syndrome virus.
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Arteriviridae; Arterivirus.
REFERENCE 1 (bases 1 to 4374)
AUTHORS Bautista,E.M. and McGruder,E.D.
TITLE Cloning and expression of PRRSV ORF1b and demonstration and
characterization of its NTPase activity
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4374)
AUTHORS Bautista,E.M. and McGruder,E.D.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Biology Research and Development, Elanco
Animal Health, a Division of Eli Lilly and Company, 2001 West Main
St, Greenfield, IN 46140, USA
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 17:03:44 ; Search time 23.9 Seconds
(without alignments)
52.688 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	17	20	AA02537 Peptide derived fr
2	81	100.0	623	20	AA02540 Protein encoded by
3	78	96.3	100	20	AA02542 Protein encoded by
4	78	96.3	123	20	AA02543 Protein encoded by
5	78	96.3	256	20	AA02538 Protein encoded by
6	78	96.3	630	20	AA02541 Protein encoded by
7	70	86.4	517	21	AA03857 Arabidopsis thalia
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16	70	86.4	587	22	AAE01892 Arabidopsis thalia
17	66	81.5	572	22	AAE01892 Arabidopsis thalia
18	66	81.5	572	22	AAE01892 Arabidopsis thalia
19	62	76.5	138	20	AA02544 Amino acid sequenc
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ALIGNMENTS

RESULT 1
AA02537
ID AAY02537 standard; Peptide; 17 AA.
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AC AAY02537;
XX
DT 16-JUL-1999 (first entry)
XX
DE Peptide derived from a protein causing growth inhibition.
DE Rht gene; homologue: Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol.
XX
XX Unidentified.
XX OS.
XX PN WO9909174-A1.
XX PD 25-FEB-1999.
XX 07-AUG-1998; 98WO-GB02383.
XX 13-AUG-1997; 97GB-0017192.
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX Harberd NP, Peng J, Richards DE;
XX WPI; 1999-181040/15.
XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX

PS Claim 1; Page 53; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC a peptide derived from a protein causing growth inhibition when
CC expressed in wheat.

XX Sequence 17 AA;

Query Match 100.0%; Score 81; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.8e-08; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGKVKVRSMDMA 17

Db 1 dellaalgykvrasm 17

RESULT 2

RAY02540

ID AAY02540 standard; Protein; 623 AA.

XX AC AAY02540;

DT 16-JUL-1999 (first entry)

DE Protein encoded by wheat Rht clone 5a1 genomic sequence.

KW Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol.

OS *Triticum aestivum*.

PN WO9909174-A1.

PD 25-FEB-1999.

PF 07-AUG-1998; 98WO-GB02383.

PR 13-AUG-1997; 97GB-0017192.

PA (PLAN-) PLANT BIOSCIENCE LTD.

PI Harberd NP, Peng J, Richards DE;

DR WPI; 1999-181040/15.

DR N-PSDB; AAX36279.

XX New *Triticum aestivum* polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 8b; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be

CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is encoded by
CC the wheat Rht clone 5a1 genomic sequence.

XX Sequence 623 AA;

Query Match 100.0%; Score 81; DB 20; Length 623;

Best Local Similarity 100.0%; Pred. No. 1e-06; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGKVKVRSMDMA 17

Db 38 dellaalgykvrasm 54

RESULT 3

RAY02542

ID AAY02542 standard; Protein; 100 AA.

XX AC AAY02542;

DT 16-JUL-1999 (first entry)

DE Protein encoded by the partial sequence of the maize D8-1 allele.

KW Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; maize.

OS Zea mays.

PN WO9909174-A1.

PD 25-FEB-1999.

PF 07-AUG-1998; 98WO-GB02383.

PR 13-AUG-1997; 97GB-0017192.

PA (PLAN-) PLANT BIOSCIENCE LTD.

PI Harberd NP, Peng J, Richards DE;

DR WPI; 1999-181040/15.

DR N-PSDB; AAX36281.

XX New *Triticum aestivum* polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 11b; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is encoded by
CC the partial sequence of the maize D8-1 allele.

```

SQ Sequence 100 AA;
Query Match 96.3%; Score 78; DB 20; Length 100;
Best Local Similarity 94.1%; Pred. No. 4.7e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRSDMA 17
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Db 34 dellaalgykvrssdma 50

RESULT 4
AA02543
ID AAY02543 standard; Protein; 123 AA.
XX AC AAY02543;
XX DT 16-JUL-1999 (first entry)
XX DE Protein encoded by the partial sequence of the maize D8-2023 allele.
XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
XX KW paclobutrazol; maize.
XX OS Zea mays.
XX PN WO9509174-A1.
XX PD 25-FEB-1999.
XX PF 07-AUG-1998; 98WO-GB02383.
XX PR 13-AUG-1997; 97GB-0017192.
XX PA (PLAN-) PLANT BIOSCIENCE LTD.
XX PI Harberd NP, Peng J, Richards DE;
XX DR N-PSDB; AAX36282.
XX CC The specification describes polypeptides encoded by the Rht gene (and
XX CC its homologues) that, when expressed in Triticum aestivum, inhibit
XX CC growth of the plant. This growth inhibition is antagonised by
XX CC gibberellin. The products can be used to provide Rht expression in
XX CC plants, conferring a dwarf phenotype on a plant which is correctable
XX CC by treatment with gibberellin. In addition, the products can be
XX CC used to produce Rht mutant plants which are dwarfed compared with
XX CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
XX CC may be made by knocking out Rht or the relevant homologous gene in
XX CC the plant of interest. Plants may be made which are resistant to
XX CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
XX CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
XX CC dwarf but let crop plants grow tall. The present sequence is encoded by
XX CC the partial sequence of the maize D8-2023 allele.
XX SQ Sequence 123 AA;

Query Match 96.3%; Score 78; DB 20; Length 123;
Best Local Similarity 94.1%; Pred. No. 6e-07;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRSDMA 17
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SQ Sequence 123 AA;

Query Match 96.3%; Score 78; DB 20; Length 256;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRSDMA 17
|||||
Db 38 dellaalgykvrssdma 54

RESULT 6
AA02541
ID AAY02541 standard; Protein; 630 AA.
XX AC AAY02541;

```

Db 22 dellaalgykvrssdma 38

RESULT 5

AA02538
ID AAY02538 standard; Protein; 256 AA.

XX AC AAY02538;
XX DT 16-JUL-1999 (first entry)
XX DE Protein encoded by rice EST D39460 sequence.

XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
XX KW paclobutrazol; rice; expressed sequence tag; EST.

XX OS Oryza sativa.

XX PN WO9909174-A1.

XX PD 25-FEB-1999.

XX PF 07-AUG-1998; 98WO-GB02383.

XX PR 13-AUG-1997; 97GB-0017192.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Harberd NP, Peng J, Richards DE;

XX DR N-PSDB; AAX36277.

XX CC New Triticum aestivum polynucleotides - encode a polypeptide which
XX CC provides inhibition of the growth of plants, which inhibition is
XX CC antagonised by gibberellin, used to confer a dwarf phenotype

XX PS Claim 12; Fig 6b; 88pp; English.

XX CC The specification describes polypeptides encoded by the Rht gene (and
XX CC its homologues) that, when expressed in Triticum aestivum, inhibit
XX CC growth of the plant. This growth inhibition is antagonised by
XX CC gibberellin. The products can be used to provide Rht expression in
XX CC plants, conferring a dwarf phenotype on a plant which is correctable
XX CC by treatment with gibberellin. In addition, the products can be
XX CC used to produce Rht mutant plants which are dwarfed compared with
XX CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
XX CC may be made by knocking out Rht or the relevant homologous gene in
XX CC the plant of interest. Plants may be made which are resistant to
XX CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
XX CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
XX CC dwarf but let crop plants grow tall. The present sequence is encoded by
XX CC wheat Rht gene.

XX SQ Sequence 256 AA;

Query Match 96.3%; Score 78; DB 20; Length 256;
Best Local Similarity 94.1%; Pred. No. 1.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRSDMA 17

|||||
Db 38 dellaalgykvrssdma 54

RESULT 6

AA02541
ID AAY02541 standard; Protein; 630 AA.

XX AC AAY02541;

XX 16-JUL-1999 (first entry)
 XX DT Protein encoded by maize lal genomic clone sequence.
 XX DE
 XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
 KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 KW paclobutrazol; maize.
 XX OS
 XX OS Zea mays.
 XX WO9909174-A1.
 XX 25-FEB-1999.
 XX PF 07-AUG-1998; 98WO-GB02383.
 XX 13-AUG-1997; 97GB-0017192.
 XX PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX PI Harberd NP, Peng J, Richards DE;
 XX WPI; 1999-181040/15.
 XX N-PSDB; AAX36280.
 XX New Triticum Aestivum polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is
 PT antagonised by gibberellin, used to confer a dwarf phenotype
 XX Disclosure; Fig 9b; 88pp; English.
 XX The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in Triticum Aestivum, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence is encoded by
 CC the maize lal genomic clone sequence.
 XX Sequence 630 AA;
 SQ

Query Match 96.3%; Score 78; DB 20; Length 630;
 Best/Local Similarity 94.1%; Pred. No. 3.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DELLAALGYKVRASDMA 17
 Db 38 dellaaalgykvrssdma 54
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RESULT 7
 AAG38577
 ID AAG38577 standard; Protein: 517 AA.
 XX AAG38577;
 AC
 XX 18-OCT-2000 (first entry)
 DT Arabidopsis thaliana protein fragment SEQ ID NO: 47612.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 47612.
 XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX

OS Arabidopsis thaliana.
 XX EPI033405-A2.
 XX 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
 XX 05-MAR-1999; 99US-0123180.
 XX 09-MAR-1999; 99US-0123548.
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 XX 25-MAR-1999; 99US-0126264.
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Query Match 86.4%; Score 70; DB 21; Length 517;
Best Local Similarity 82.4%; Pred. No. 9.4e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 12 dellavlgkyvrssema 28

RESULT 8

AAG38576
ID AAG38576 standard; Protein; 518 AA.

XX AAG38576;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 47611.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 99US-0121825.
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99US-0148341.
99US-0148565.
99US-0148684.
99US-0149368.
99US-0149175.
99US-0149426.
99US-0149722.
99US-0149723.
99US-0149929.
99US-0149902.
99US-0149902.
99US-0149930.
99US-0150566.
99US-0150884.
99US-0151065.
99US-0151066.
99US-0151080.
99US-0151303.
99US-0151438.
99US-0151930.
99US-0152363.
99US-0153070.
99US-0153758.
99US-0154018.
99US-0154039.
99US-0154779.
99US-0155139.
99US-0155486.
99US-0155659.
99US-0156458.


```

PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161362.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 86.4%; Score 70; DB 21; Length 518;
Best Local Similarity 82.4%; Pred. No. 9.5e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
Db 13 dellavlgkvrssma 29

RESULT 9
AAB28575
ID AAB28575 standard; Protein; 531 AA.
XX
AC AAB28575;
XX
DT 09-FEB-2001 (first entry)
XX
DE Arabidopsis SCLa2.
XX
KW Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL;
KW transgenic plant; cell division; molecular marker; herbicide resistance;
KW salt resistance; pathogen resistance; insect resistance.
XX
OS Arabidopsis thaliana.
XX
PN WO200053723-A2.
XX
PD 14-SEP-2000.
XX
PF 07-MAR-2000; 2000WO-US05875.
XX
PR 10-MAR-1999; 99US-0265585.
XX
PA (UYNV ) UNIV NEW YORK STATE.
XX
PI Benfey PN, Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysch L;
PI Helariutta Y, Bruce W, Lim J;

PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161362.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 86.4%; Score 70; DB 21; Length 531;
Best Local Similarity 82.4%; Pred. No. 9.7e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
Db 27 dellavlgkvrssma 43

RESULT 10
AAN30792
ID AAN30792 standard; Protein; 532 AA.
XX
AC AAN30792;
XX
DT 19-MAR-1998 (first entry)
XX
DE Arabidopsis thaliana gibberellin insensitivity gai gene product.
XX
KW Gibberellin insensitivity; gai; plant growth inhibition;
KW dwarf phenotype; lodging resistance; increased yield;
KW flowering regulation; bolting inhibition; spinach; lettuce;
KW antibody; identification; probe; primer; antisense; sense;
KW expression regulation; co-suppression; rice;
KW Bakane disease resistance.
XX
OS Arabidopsis thaliana.
XX
PN WO9729123-A2.
XX
PD 14-AUG-1997.
XX
PF 12-FEB-1997; 97WO-GB00390.
XX
PR 12-FEB-1996; 96GB-0002796.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Carol P, Harberd NP, Peng J, Richards DE;
XX
WPI; 1997-415295/38.
DR N-PSDB; AAT91937.
XX
PT Nucleic acid encoding gibberellin inhibitor GAI and related

```

antisense sequences - used to create tall, or particularly, dwarf plants, especially crops such as maize, rice and wheat
 Claim 1; Fig 4; 76pp; English.

The present sequence is the Arabidopsis thaliana gibberellin insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype that is insensitive to GA. Manipulating gai and GAI expression can produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tailor the degree of dwarfism and GA sensitivity to particular crops or situations.

SQ Sequence 532 AA;

Query Match 86.4%; Score 70; DB 18; Length 532;
 Best Local Similarity 82.4%; Pred. No. 9.7e-05;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DELLAALGKYKVRSDMA 17
 ||||| |||||:|:|
 Db 27 dellavlgkyvrssma 43

RESULT 11

AAE02545
 ID AAE02545 standard; Protein: 532 AA.

XX AC AAE02545;

DT 10-AUG-2001 (first entry)

DE A. thaliana transcription factor G308.

KW plant transcription factor; phenotype: sugar sensing characteristic;
 KW transgenic plant; plant yield; growth; germination; photosynthesis;
 KW glyoxylate metabolism; respiration; pathogen response; wounding response;
 KW cell cycle regulation; pigmentation; flowering; senescence; physiology;
 KW storage organ; metabolism.

OS Arabidopsis thaliana.

FH Key Location/Qualifiers
 FT Domain 270..274
 FT /note= "Conserved domain"

PN WO200135725-A1.

XX PD 25-MAY-2001.

XX PF 14-NOV-2000; 2000WO-US31414.

PR 17-NOV-1999; 99US-0166228.

PR 17-APR-2000; 2000US-0197899.

PR 22-AUG-2000; 2000US-0227439.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

PA (JIAN/) JIANG C.

PA (HEAR/) HEARD J.

PA (PINE/) PINEDA O.

PA (PILG/) PILGRIM M.

PA (ADAM/) ADAM L.

PA (RIEC/) RIECHMANN J L.
 PA (YUGG/) YU G.
 PA (SAMA/) SAMAHA R.

XX Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
 PI Yu G, Samaha R;

DR WPI; 2001-335977/35.

DR N-PSDB; AAD06646.

XX Nucleic acids encoding plant transcription factor polypeptides, useful
 PT for altering the sugar sensing characteristics of plants and increasing
 PT yield, e.g. corn, potato and cotton plants -

PS Claim 4; Page 74-76; 151pp; English.

XX The patent relates to polynucleotides encoding 35 plant transcription
 CC factors which may be used to modify phenotype associated with a plant's
 CC sugar sensing characteristics and increasing yield when their expression
 CC level is altered. Sugars are central regulatory molecules that control
 CC aspects of physiology, metabolism and development. Therefore the cDNAs
 CC and proteins of the invention are useful for modifying the growth and
 CC germination rates of plants, photosynthesis, glyoxylate metabolism,
 CC respiration, starch and sucrose synthesis and degradation, pathogen
 CC response, wounding response, cell cycle regulation, pigmentation,
 CC flowering and senescence of plants and for modifying sink-source
 CC relationships in seeds, tubers, roots, and other storage organs leading
 CC to an increase in yield. The transcription factor polynucleotides and
 CC polypeptides may be used to alter the structure and developmental
 CC characteristics of plants such as soybean, wheat, corn, potato, cotton,
 CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
 CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
 CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
 CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
 CC tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
 CC The present sequence is an Arabidopsis thaliana transcription factor.

SQ Sequence 532 AA;

Query Match 86.4%; Score 70; DB 22; Length 532;

Best Local Similarity 82.4%; Pred. No. 9.7e-05;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DELLAALGKYKVRSDMA 17

||||| |||||:|:|

Db 27 dellavlgkyvrssma 43

RESULT 12

AAE01907

ID AAE01907 standard; Protein: 532 AA.

XX AC AAE01907;

XX 31-JUL-2001 (first entry)

XX Arabidopsis thaliana transcription factor, G308.

XX Transcription factor; biochemical characteristic; controlling element;
 KW structural characteristic; developmental characteristic; gene therapy;
 KW agricultural biotechnology; plant trait modification.

XX Arabidopsis thaliana.

FH Key Location/Qualifiers
 FT Domain 270..274
 FT /label= Conserved_domain

XX WO200136597-A1.

PN 25-MAY-2001.

PF 14-NOV-2000; 2000WO-US31344.
XX
PR 17-NOV-1999; 99US-0166228.
PR 17-APR-2000; 2000US-0197899.
PR 22-AUG-2000; 2000US-0227439.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (CREE/) CREELMAN R.
PA (YUGG/) YU G.
PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (HEAR/) HEARD J.
PA (SAMA/) SAMAHA R.
PA (PILG/) PILGRIM M.
PA (PINE/) PINEDA O.
PA (JIAN/) JIANG C.
XX
XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
PI Pilgrim M, Pineda O, Jiang C;
XX
XX WPI: 2001-335999/35.
DR N-PSDB; AAD05791.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the biochemical characteristics of plants e.g. corn,
PT potato and cotton plants -
XX
XX Claim 4; Page 114-115; 127pp; English.
XX
CC The present sequence is Arabidopsis thaliana transcription factor,
CC G308, a homologue of G307. The transcription factor is used for altering
CC a plant's biochemical characteristics. The transcription factor may be
CC used to alter the structure and developmental characteristics of plants
CC such as soybean, wheat, corn, potato, cotton, rice, oilseed rape,
CC sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry,
CC strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber,
CC eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas,
CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,
CC watermelon, rosaceous fruits and/or vegetable brassicas. Transcription
CC factors are key controlling elements of biological pathways and altering
CC expression levels of 1 or more transcription factors can change entire
CC biological pathways in an organism. Therefore manipulating transcription
CC factor levels in plants offers great potential in agricultural
CC biotechnology for modifying a plant's traits. Transcription factor cDNA
CC is useful in gene therapy.
XX
XX Sequence 532 AA;
SQ

Query Match 86.4%; Score 70; DB 22; Length 532;
Best Local Similarity 82.4%; Pred. No. 9.7e-05;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 DELLALGYKVRASDMA 17
Db 27 dellavlgkyvrssema 43
RESULT 13
AAG38575
ID AAG38575 standard; Protein; 533 AA.
XX
XX AAG38575;
AC
XX
DT 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 47610.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS


```

PR 10-MAR-1999; 99US-0265585.
XX (UYN ) UNIV NEW YORK STATE.
PA Benfey PN, Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysch L;
PI Helariutta Y, Bruce W, Lim J;
XX WPI; 2000-594315/56.
DR N-PSDB; AAC65291.
XX
XX Scarecrow gene useful for producing transgenic plants expressing genes
PT whose product increases starch, lignin or cellulose biosynthesis and
PT confers herbicide, pathogen or insect resistance -
XX
XX Claim 14; Fig 13; 200pp; English.
XX
XX The present sequence is given in a specification relating to the
CC structure and function of a regulatory gene, SCARECROW (SCR).
CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (WHIID) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem
CC development and gravitropism of stem or hypocotyl is altered. Cell
CC division is increased or decreased in roots resulting in thicker or
CC thinner root development. The transgenic plants are useful for expressing
CC a gene of interest encoding a gene product that confers herbicide, salt,
CC pathogen or insect resistance in root or embryos and genes encoding
CC starch, lignin or cellulose biosynthesis in shoots. The SCR gene also
CC confers less susceptibility to lodging in the transgenic plants than a
CC wild-type plant. SCR gene sequences are also useful as molecular markers
CC for a quantitative trait e.g. root or gravitropism trait in molecular
XX breeding of crop plants.
XX
XX Sequence 587 AA;
SQ

Query Match 86.4%; Score 70; DB 21; Length 587;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
Db ||||| |||||:|:|
44 dellavigykvrsema 60

RESULT 15
AAE02560
ID AAE02560 standard; Protein; 587 AA.
XX
XX AAE02560;
AC
XX
XX 10-AUG-2001 (first entry)
DT
XX
XX A. thaliana transcription factor G308 homolog, G307.
DE
XX
XX Plant transcription factor; phenotype; sugar sensing characteristic;
KW transgenic plant; plant yield; growth; germination; photosynthesis;
KW glyoxylate metabolism; respiration; pathogen response; wounding response;
KW cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW storage organ; metabolism.
XX
XX Arabidopsis thaliana.
OS
XX
XX Key Location/Qualifiers
FH Domain 323..339
FT /note= "Conserved domain"
FT
XX
XX WO200135725-A1.
PN
XX
XX 25-MAY-2001.
PD
XX
XX 14-NOV-2000; 2000WO-US31414.
XX
XX

```

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PR 17-NOV-1999; 99US-0166228.
PR 17-APR-2000; 2000US-0197899.
PR 22-AUG-2000; 2000US-0227439.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J.
PA (PINE/) PINEDA O.
PA (PILG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (SAMA/) SAMAHA R.
XX
XX Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
PI Yu G, Samaha R;
XX
XX WPI; 2001-335977/35.
DR N-PSDB; AAD06661.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the sugar sensing characteristics of plants and increasing
PT yield, e.g. corn, potato and cotton plants -
XX
XX Claim 4; Page 115-117; 151pp; English.
XX
XX The patent relates to polynucleotides encoding 35 plant transcription
CC factors which may be used to modify phenotype associated with a plant's
CC sugar sensing characteristics and increasing yield when their expression
CC level is altered. Sugars are central regulatory molecules that control
CC aspects of physiology, metabolism and development. Therefore the cDNAs
CC and proteins of the invention are useful for modifying the growth and
CC germination rates of plants, photosynthesis, glyoxylate metabolism,
CC respiration, starch and sucrose synthesis and degradation, pathogen
CC response, wounding response, cell cycle regulation, pigmentation,
CC flowering and senescence of plants and for modifying sink-source
CC relationships in seeds, tubers, roots, and other storage organs leading
CC to an increase in yield. The transcription factor polynucleotides and
CC polypeptides may be used to alter the structure and developmental
CC characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
CC The present sequence is a homolog of Arabidopsis thaliana transcription
XX factor.
XX
XX Sequence 587 AA;
SQ

Query Match 86.4%; Score 70; DB 22; Length 587;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
Db ||||| |||||:|:|
44 dellavigykvrsema 60

Search completed: December 19, 2001, 17:07:10
Job time: 206 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 19, 2001, 17:05:49 ; Search time 12.86 Seconds
(without alignments)
100.697 Million cell updates/sec

Title: US-09-485-529-104

Perfect score: 81

Sequence: 1 DELLAALGYKVRASDMA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PTR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	86.4	511	2 G96688	hypothetical prote
2	70	86.4	523	2 T51475	RGA-like protein -
3	70	86.4	533	2 H86282	protein F1086.34 [
4	70	86.4	587	2 D84426	hypothetical prote
5	46	56.8	495	2 C71679	UDP-N-acetylmuram
6	45	55.6	257	2 T10758	mandelonitrile lya
7	44	54.3	466	2 B69610	carboxy-terminal p
8	43	53.1	640	2 E64116	exodeoxyribonuclea
9	42	51.9	263	2 T01149	probable acetone-c
10	42	51.9	516	2 E96839	hypothetical prote
11	41	50.6	272	2 C72498	probable stress pr
12	41	50.6	311	2 A75047	2-ketovallate oxi
13	41	50.6	314	2 B71114	probable ferredoxi
14	41	50.6	454	2 B70418	UDP-N-acetylmuram
15	41	50.6	463	2 D81960	ATP-dependent DNA
16	41	50.6	469	2 B81201	UDP-N-acetylmuram
17	41	50.6	484	2 C84955	UDP-N-acetylmuram
18	41	50.6	491	1 CE6CAM	UDP-N-acetylmuram
19	41	50.6	491	2 G85491	hypothetical prote
20	41	50.6	506	2 A81777	UDP-N-acetylmuram
21	41	50.6	550	2 T37519	probable amino aci
22	41	50.6	1002	2 T07292	FUN12 protein - ye
23	40	49.4	96	2 G83600	hypothetical prote
24	40	49.4	330	2 A83417	probable oxidoredu
25	40	49.4	477	2 E82763	UDP-N-acetylmuram
26	40	49.4	480	2 D83094	UDP-N-acetylmuram
27	40	49.4	700	2 T49445	adrenoleukodystrop
28	40	49.4	957	2 T10633	hypothetical prote
29	39	48.1	82	2 A72274	hypothetical prote

30	39	48.1	136	2 H75570	conserved hypothet
31	39	48.1	141	2 T02428	probable (S)-aceto
32	39	48.1	188	2 A71186	probable ribosomal
33	39	48.1	194	2 S76919	hypothetical prote
34	39	48.1	250	2 F83609	hypothetical prote
35	39	48.1	263	2 T01151	probable acetone-c
36	39	48.1	294	2 A49932	2,2',3-trihydroxyb
37	39	48.1	294	2 H81448	probable molybdenu
38	39	48.1	311	2 T45086	pyruvate synthase
39	39	48.1	377	2 F82201	spermidine/putresc
40	39	48.1	378	2 A40840	spermidine/putresc
41	39	48.1	378	2 F85683	hypothetical prote
42	39	48.1	381	2 B64118	spermidine/putresc
43	39	48.1	481	2 C71338	probable UDP-N-ace
44	39	48.1	604	2 B84221	hypothetical prote
45	39	48.1	643	2 T19135	cholecystokin in ty

ALIGNMENTS

RESULT 1

G96688

hypothetical protein T27F4.10 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: G96688

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
anssen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
J. Biol. Chem. 274, 11111-11118, 1999

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: G96688

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-511 <STO>

A:Cross-references: GB:AE005173; NID:gl0092507; PIDN:AAG12907.1; GSPDB:GN00141

C:Genetics:

A:Gene: T27F4.10

A:Map position: 1

Query Match 86.4%; Score 70; DB 2; Length 511;
Best Local Similarity 82.4%; Pred. No. 0.00017;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17

||||| ||||||| |||||

Db 32 DELLVWLGYKVRSSDMA 48

RESULT 2

T51475

RGA-like protein - Arabidopsis thaliana

N:Alternate names: protein K3M16_60

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51475

R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.;

submitted to the Protein Sequence Database, August 2000

A:Reference number: Z25394

A:Accession: T51475

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-523 <SAT>

A:Cross-references: EMBL:AL391150

A:Experimental source: cultivar Columbia; BAC clone K3M16

C:Genetics:
A:Map position: 5
A:Note: K3M16_60

Query Match 86.4%; Score 70; DB 2; Length 523;

Best Local Similarity 82.4%; Pred. No. 0.00017;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DELLAALGKVRASDMA 17

Db 34 DEFLAVLGKVRSDMA 50

RESULT 3

H86282 protein F10B6.34 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: H86282

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H86282

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-533 <STO>

A:Cross-references: GB:AE005172; NID:98778219; PIDN:AAF79228.1; GSPDB:GN00141

C:Genetics:

A:Gene: F10B6.34

A:Map position: 1

Query Match 86.4%; Score 70; DB 2; Length 533;

Best Local Similarity 82.4%; Pred. No. 0.00018;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGKVRASDMA 17

Db 28 DEFLAVLGKVRSDMA 44

RESULT 4

DB4426

hypothetical protein At2g01570 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: DB4426

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.V.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: DB4426

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-587 <STO>

A:Cross-references: GB:AE002093; NID:93785986; PIDN:AAC67333.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g01570

A:Map position: 2

Query Match 86.4%; Score 70; DB 2; Length 587;

Best Local Similarity 82.4%; Pred. No. 0.00019;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGKVRASDMA 17

Db 44 DEFLAVLGKVRSDMA 60

RESULT 5

C71679

UDP-n-acetylmuramate--alanine ligase (murC) RP247 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000

C:Accession: C71679

R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499

A:Accession: C71679

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-495 <AND>

A:Cross-references: GB:AJ235271; GB:AJ235269; NID:93868717; PIDN:CAAL4709.1; PID:9386

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: murC; RP247

C:Superfamily: UDP-N-acetylmuramate--alanine ligase

Query Match 56.8%; Score 46; DB 2; Length 495;

Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ELLAALGKVRASDM 16

Db 31 EILHLGKVGSGDL 45

RESULT 6

T10758

mandelonitrile lyase (EC 4.1.2.10) - Para rubber tree

N:Alternate names: hydroxynitrile lyase

C:Species: Hevea brasiliensis (Para rubber tree)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10758

R:Hasslach, M.; Schall, M.; Hayn, M.; Griengl, H.; Kohlwein, S.D.; Schwab, H.

J. Biol. Chem. 271, 5884-5891, 1996

A:Title: Molecular-cloning of the full-length cDNA of (s)-hydroxynitrile lyase from h

n active-site residue.

A:Reference number: 203416; MUID:96215058

A:Accession: T10758

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-257 <HAS>

A:Cross-references: EMBL:U40402; NID:91223883; PIDN:AAC49184.1; PID:91223884

A:Experimental source: leaves

C:Genetics:

A:Gene: hml

C:Function:

A:Description: catalyzes the conversion of mandelonitrile to benzaldehyde and cyanide

A:Note: involved in the biodegradation of cyanogenic glycosides; also catalyzes the s

C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 55.6%; Score 45; DB 2; Length 257;

Best Local Similarity 66.7%; Pred. No. 2.4;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LLAALGKVRASDMA 17

Db 25 LLEALGHKVTALDLA 39

RESULT 7
B69610
carboxy-terminal processing proteinase ctpA (EC 3.4.99.-) - Bacillus subtilis
N:Alternate names: tail-specific endopeptidase Prc
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: B69610; JG5744
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scallan
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:9804033
A:Accession: B69610
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-466 <KUN>
A:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13850.1; PID:g2634351
A:Experimental source: strain 168
R:Marasco, R.; Varcamonti, M.; Ricca, E.; Sacco, M.
Gene 183, 149-152, 1996
A:Title: A new Bacillus subtilis gene with homology to Escherichia coli prc.
A:Reference number: JC5744; MUID:97149292
A:Accession: JC5744
A:Molecule type: DNA
A:Residues: 1-297, 'RSRNTGRC', 306-466 <MAR>
A:Cross-references: EMBL:X98341; NID:gl402943; PIDN:CAA66987.1; PID:gl402944
A:Experimental source: strain PY17
C:Comment: This protein is presumed to be involved in cleavage of the carboxyl-terminal
C:Genetics:
A:Gene: ctpA
A:Start codon: TTG
C:Superfamily: carboxyl-terminal processing proteinase
C:Keywords: hydrolase

Query Match 54.3%; Score 44; DB 2; Length 466;
Best Local Similarity 53.3%; Pred. No. 6.6;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 ELAALGYKVRASDM 16
DB 394 KMLKALGYKVKVNSM 408
::: |||||:::
DB 394 KMLKALGYKVKVNSM 408

RESULT 8
E64116
exodeoxyribonuclease V 67K chain homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: E64116
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.I.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: E64116
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-640 <TTGR>
A:Cross-references: GB:U32811; GB:I42023; NID:gi574774; PIDN:AAC22967.1; PID:gi574782; T

C:Superfamily: exodeoxyribonuclease V 67K chain

Query Match 53.1%; Score 43; DB 2; Length 640;
Best Local Similarity 69.2%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 LLAALGYKVRASD 15
DB 355 LLATGYKVEGSD 367
::: |||||:::
DB 355 LLATGYKVEGSD 367

RESULT 9
T01149
probable acetone-cyanohydrin lyase [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F26B6.25
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01149; G84626
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
submitted to the EMBL Data Library, June 1998
A:Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A:Reference number: Z14198
A:Accession: T01149
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-263 <ROU>
A:Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242721
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: G84626
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <SOT>
A:Cross-references: GB:AE002093; NID:g3242721; PIDN:AAC23773.1; GSPDB:GN00139
C:Genetics:
A:Gene: F26B6.25; At2g23600
A:Map position: 2
A:Introns: 125/3; 170/3
C:Superfamily: tropinesterase

Query Match 51.9%; Score 42; DB 2; Length 263;
Best Local Similarity 60.0%; Pred. No. 8.4;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 3 LLAALGYKVRASDMA 17
DB 29 LLEALGHRVTALDLA 43
::: |||||:::
DB 29 LLEALGHRVTALDLA 43

RESULT 10
E96839
hypothetical protein F23A5.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96839
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marzia
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719

A:Accession: E96839
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005173; NID:g503282; PIDN:AAF14658.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F23A5.6
 A:Map position: 1

Query Match 51.9%; Score 42; DB 2; Length 516;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DELAALGKVRASDM 16
 |||:||||:|:|:
 DB 17 DELAALNVRKASSL 32

RESULT 11

C72498
 probable stress protein APE1961 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: C72498
 R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; MUID:99310339
 A:Accession: C72498
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-272 <KAW>
 A:Cross-references: DBJ:AP000063; NID:g5105654; PIDN:BAA80971.1; PID:g5105659
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1961
 C:Superfamily: aldehyde reductase

Query Match 50.6%; Score 41; DB 2; Length 272;
 Best Local Similarity 37.5%; Pred. No. 13;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DELAALGKVRASDM 16
 |||:||||:|:|:
 DB 250 DELSLGWRKLPEDI 265

RESULT 12

A75047
 2-ketoglutarate oxidoreductase chain vorb (EC 1.-.-.-) (vor) PAB1473 - Pyrococcus abyssi
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: A75047
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A:Reference number: A75001
 A:Accession: A75047
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-311 <KAW>
 A:Cross-references: GB:AJ748287; GB:AL096836; NID:g5458657; PIDN:CAB50270.1; PID:g545878
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: PAB1473
 C:Superfamily: pyruvate synthase beta chain
 C:Keywords: oxidoreductase

Query Match 50.6%; Score 41; DB 2; Length 311;

Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LAALGKVRASD 15
 ||||||:|
 DB 90 LKALGKVKGED 101

RESULT 13

B71114
 probable ferredoxin oxidoreductase beta subunit - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 C:Accession: B71114
 R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137
 A:Accession: B71114
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Residues type: DNA
 A:Residues: 1-314 <KAW>
 A:Cross-references: NID:g3236130; PIDN:BAA29772.1; PID:g3237089
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
 C:Genetics:
 A:Gene: PH0681
 C:Superfamily: pyruvate synthase beta chain

Query Match 50.6%; Score 41; DB 2; Length 314;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LAALGKVRASD 15
 ||||||:|
 DB 93 LKALGKVKGED 104

RESULT 14

B70418
 UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
 C:Accession: B70418
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; V. Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666
 A:Accession: B70418
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-454 <AOQ>
 A:Cross-references: NID:g2983763; PIDN:AAC07323.1; PID:g2983764; GB:AE00
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: murC
 C:Superfamily: UDP-N-acetylmuramate--alanine ligase
 C:Keywords: ligase

Query Match 50.6%; Score 41; DB 2; Length 454;
 Best Local Similarity 43.8%; Pred. No. 22;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 ELAALGKVRASDMA 17
 ::|:|||||:|:|:
 DB 24 QILLEGKVKSGSDIS 39

RESULT 15

D81960
ATP-dependent DNA helicase NMA0433 [imported] - Neisseria meningitidis (strain Z2491 serotype 4) [NCBI]
C:Species: Neisseria meningitidis
C:date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: D81960
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, P.H.; Holtroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A.L.; White, O.; Barrell, B.G.; Haywood, V.E.; et al.
Nature 404, 502-506, 2000
A:title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: AB1775; GUID:2022556
A:Accession: D81960
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83732.1; PID:g737918
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: hrpA'; NMA0433

```
Query Match      50.6%; Score 41; DB 2; Length 463;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2  ELLAALGYKVRASD 15
      | : : | | | | : |
Db     131 EIGSAVGKVRFTD 144
```

Search completed: December 19, 2001, 17:07:48
Job time: 119 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 17:07:34 ; Search time 10.2 seconds
(without alignments)
61.108 Million cell updates/sec

Title: US-09-485-529-104

Perfect score: 81

Sequence: 1 DELLAALGYKVRASDMA 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	46	56.8	495	1 MURC_RICPR	Q92DS8 rickettsia
2	45	55.6	257	1 HNL_HEYBR	P52704 hevea bras
3	43	53.1	640	1 EX5A_HAEIN	P45158 haemophilus
4	41	50.6	311	1 VORE_PYRAB	Q9UVZ2 pyrococcus
5	41	50.6	311	1 VORE_PYRHO	O58414 pyrococcus
6	41	50.6	454	1 MURC_AQUAE	O67373 aquifex aeo
7	41	50.6	484	1 MURC_BUCAI	P57310 buchnera ap
8	41	50.6	491	1 MURC_ECOLI	P17952 escherichia
9	41	50.6	550	1 YAO8_SCHPO	Q10087 schizosacch
10	41	50.6	1002	1 IF2P_YEAST	P39730 saccharomyc
11	39	48.1	188	1 RL5_PYRHO	O59431 pyrococcus
12	39	48.1	293	1 DBFE_PSEPA	P47243 pseudomonas
13	39	48.1	311	1 VORE_PYRFU	O51802 pyrococcus
14	39	48.1	378	1 POT4_ECOLI	P23858 escherichia
15	39	48.1	381	1 POT4_HAEIN	P45171 haemophilus
16	39	48.1	481	1 MURC_TREPA	O83361 treponema p
17	38	46.9	273	1 FOLD_MYCGE	P47259 mycoplasma
18	38	46.9	325	1 THIL_ECOLI	P77785 escherichia
19	38	46.9	483	1 MURC_BUCAP	O51926 buchnera ap
20	38	46.9	516	1 YJJI_ECOLI	P37342 escherichia
21	38	46.9	617	1 VG31_BPMD2	O64225 mycobacteri
22	38	46.9	638	1 SYT2_BACSU	P18256 bacillus su
23	38	46.9	665	1 TKT_BUCAI	P57195 buchnera ap
24	38	46.9	705	1 RNR_AQUAE	O67834 aquifex aeo
25	38	46.9	1022	1 SC44_RICCN	Q26558 rickettsia
26	38	46.9	1079	1 IF2P_SCHPO	O10251 schizosacch
27	38	46.9	1538	1 GLSF_PORPU	P51375 porphyra pu
28	38	46.9	3859	1 RPOA_LELV	Q04561 lelystad vi
29	37	45.7	130	1 Y73A_ARCFU	P58014 archaeoglob
30	37	45.7	146	1 YPV9_METTF	P29586 methanobact
31	37	45.7	394	1 SYVC_YEAST	P36421 saccharomyc
32	37	45.7	455	1 AROA_AGRSP	Q9r4e4 agrobacteri
33	37	45.7	515	1 UDPE_NPVSL	Q88168 spodoptera

34	37	45.7	544	1 PYRG_AZOBR	P28595 azospirillum
35	37	45.7	554	1 HYES_HUMAN	P34913 homo sapien
36	37	45.7	583	1 IF2P_HALHA	O93625 halobacteri
37	37	45.7	1300	1 HRPA_ECOLI	P43329 escherichia
38	37	45.7	1304	1 HRPA_HAEIN	P45018 haemophilus
39	36	44.4	238	1 VG35_HSVII	Q00109 ictalurid h
40	36	44.4	283	1 NAT_MYCTU	P96848 mycobacteri
41	36	44.4	292	1 HEM3_METJA	O57989 methanococc
42	36	44.4	395	1 METC_BORAV	O07703 bordetella
43	36	44.4	401	1 SYVC_SCHPO	O14055 schizosacch
44	36	44.4	475	1 MURC_HAEIN	P45066 haemophilus
45	36	44.4	534	1 IF2P_SULAC	P95691 sulfolobus

ALIGNMENTS

RESULT	1				
MURC_RICPR					
ID	MURC_RICPR	STANDARD;	PRT;	495	AA.
AC	Q92DS8;				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-				
DE	ACETYLMURAMOYL-L-ALANINE SYNTHETASE).				
GN	MURC OR RP247.				
OS	Rickettsia prowazekii.				
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;				
OC	Rickettsiaceae; Rickettsiae; Rickettsia.				
OX	NCBI_TaxID=782;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MADRID E;				
RX	MEDLINE=99039499; PubMed=9823893;				
RA	Andersson S.G.E., Zomorodipour A., Andersson J.O.,				
RA	Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,				
RA	Eriksson A.-S., Winkler H.H., Kurland C.G.;				
RT	"The genome sequence of Rickettsia prowazekii and the origin of				
RT	mitochondria."				
RL	Nature 396:133-140(1998).				
CC	-I- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).				
CC	-I- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE -				
CC	ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.				
CC	-I- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.				
CC	-I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).				
CC	-I- SIMILARITY: BELONGS TO THE MURDEF FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL: AJ235271; CAA14709.1; -				
DR	InterPro: IPR000713; Mur_Ligase.				
DR	Pfam: PF01225; Mur_Ligase; 1.				
KW	Peptidoglycan synthesis; Cell wall; Cell division; Ligase;				
KW	ATP-binding; Complete proteome.				
FT	NP_BIND 120 126 ATP (POTENTIAL).				
SQ	SEQUENCE 495 AA; 54612 MW; 2E18464088FAD2D6 CRC64;				

Query Match 56.8%; Score 46; DB 1; Length 495;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ELIAALGYKVRASDM 16

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Db 31 EILHNLGYKVGSD 45

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RESULT 2
HNL_HEVER
ID HNL_HEVER STANDARD; PRT; 257 AA.
AC P52704;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE (S)-ACETONE-CYANOHYDRIN LYASE (EC 4.1.2.39) ((S)-HYDROXYNITRILE LYASE)
DE ((S)-HYDROXYNITRILE) (OXYNITRILASE).
GN HNL.
OS Hevea brasiliensis (Para rubber tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eumids I; Malpighiales; Euphorbiaceae; Hevea.
OX NCBI_TaxID=3981;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Leaf;
RX MEDLINE=96215058; PubMed=8621461;
RA Hasselbacher M., Schall M., Hayn M., Griengl H., Kohlwein S.D.,
RA Schwab H.;
RT "Molecular cloning of the full-length cDNA of (S)-hydroxynitrile
RT lyase from Hevea brasiliensis. Functional expression in Escherichia
RT coli and Saccharomyces cerevisiae and identification of an active
RT site residue."
RL J. Biol. Chem. 271:5884-5891(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=96434327; PubMed=8805565;
RA Wagner U.G., Hasselbacher M., Griengl H., Schwab H., Kratky C.;
RA "Mechanism of cyanogenesis: the crystal structure of hydroxynitrile
RT lyase from Hevea brasiliensis."
RL Structure 4:811-822(1996).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=99423043; PubMed=10494852;
RA Gruber K., Gugganig M., Wagner U.G., Kratky C.;
RA "Atomic resolution crystal structure of hydroxynitrile lyase from
RT Hevea brasiliensis."
RL Biol. Chem. 380:993-1000(1999).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.72 ANGSTROMS).
RX MEDLINE=20014021; PubMed=10548044;
RA Zuegg J., Gruber K., Gugganig M., Wagner U.G., Kratky C.;
RA "Three-dimensional structures of enzyme-substrate complexes of the
RT hydroxynitrile lyase from Hevea brasiliensis."
RL Protein Sci. 8:1990-2000(1999).
CC -!- FUNCTION: INVOLVED IN CYANOGENESIS, THE RELEASE OF HCN FROM
CC INJURED TISSUES. DECOMPOSES A VARIETIES OF (R) OR (S) CYANOHYDRINS
CC INTO HCN AND THE CORRESPONDING ALDEHYDES AND KETONES. THE NATURAL
CC SUBSTRATE OF THIS ENZYME IS (S)-ACETONE CYANOHYDRIN.
CC -!- CATALYTIC ACTIVITY: (S)-2-HYDROXYISOBUTYRONITRILE - CYANIDE +
CC ACETONE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- PTM: THE N-TERMINUS IS BLOCKED.
CC -!- SIMILARITY: DISTANT RELATIONSHIP WITH TYPE-B
CC CARBOXYL ESTERASE/LIPASE FAMILY.
CC -----
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CC -----
DR EMBL; U40402; AAC49184.1; -
DR PDB; 1VAS; 16-JUN-97.
DR PDB; 2VAS; 13-OCT-99.
DR PDB; 3YAS; 13-OCT-99.
DR PDB; 4YAS; 13-OCT-99.
DR PDB; 5YAS; 13-OCT-99.
PDB; 6YAS; 13-OCT-99.
PDB; 1QJ4; 10-OCT-99.
InterPro: IPR000073; Abhydrolase.
Pfam: PF00561; abhydrolase; 1.
Lyase; 3D-structure.
FT ACT_SITE 80 80
FT ACT_SITE 207 207
FT ACT_SITE 235 235
FT MUTAGEN 80 80
FT MUTAGEN 81 81
FT MUTAGEN 235 235
SQ SEQUENCE 257 AA; 29227 MW; EF4AE88717279CEB CRC64;
Query Match 55.6%; Score 45; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 LLAALGYKVRASDMA 17
Db 25 LLEALGHKVTALDLA 39
RESULT 3
EX5A_HAEIN STANDARD; PRT; 640 AA.
AC P45158;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EXODEOXYRIBONUCLEASE V ALPHA CHAIN (EC 3.1.11.5).
GN RECD OR H11322.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Felschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 269:496-512(1995).
CC -!- FUNCTION: EXHIBITS SEVERAL CATALYTIC ACTIVITIES, INCLUDING
CC ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDONUCLEASE,
CC ATP-DEPENDENT UNWINDING AND DNA-DEPENDENT ATPASE ACTIVITIES.
CC STRAND CLEAVAGE OCCURS 5' TO 3' DURING THE UNWINDING OF DUPLEX
CC DNA AT CHI SEQUENCES, WHICH LOCALLY STIMULATE RECOMBINATION
CC (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: EXONUCLEOLYTIC CLEAVAGE (IN THE PRESENCE OF
CC ATP) IN EITHER 5'-TO 3'-OR 3'-TO 5'-DIRECTION TO YIELD 5'-
CC PHOSPHOOLIGONUCLEOTIDES.
CC -!- SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
CC (BY SIMILARITY).
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DR EMBL: U32811; AAC22967.1; -.
DR HSSP: P09980; 1UAA.
DR TIGR: H11322; -.
KW Hydrolase; Nuclease; Exonuclease; Helicase; ATP-binding;
FT DNA repair; Complete proteome.
FT NP_BIND 194 201 ATP (POTENTIAL).
SQ SEQUENCE 640 AA; 72864 MW; C3C530AC398B5DA0 CRC64;

Query Match 53.1%; Score 43; DB 1; Length 640;
Best Local Similarity 69.2%; Pred. No. 6.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 LLAALGYKVRASD 15
   III IIII II
Db 355 LLATGKVGESD 367

RESULT 4
VORB_PVRAB
ID VORB_PVRAB STANDARD; PRT; 311 AA.
AC OSUVZ2;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (2-OXOISOVALERATE-
DE OXOISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
DE FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT).
GN VORB OR PAB1473.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RA Helling R.;
RT structure and evolution.
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: AJ248287; CAB50270.1; -.
DR OXidoreductase; Complete proteome.
SQ SEQUENCE 311 AA; 34759 MW; IEBE2609519DAC30 CRC64;

Query Match 50.6%; Score 41; DB 1; Length 311;
Best Local Similarity 66.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LLAALGYKVRASD 15
   I IIIIII I
Db 90 LKALGYKVGKED 101

RESULT 5
VORB_PVRHO
ID VORB_PVRHO STANDARD; PRT; 311 AA.
AC OS8414;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (2-OXOISOVALERATE-
DE OXOISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
DE OXOISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-

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DE FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT).
GN VORB OR PH0681.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: AP000003; BAA29772.1; ALT_INIT.
DR OXidoreductase; Complete proteome.
SQ SEQUENCE 311 AA; 34569 MW; E27B65877EF65813 CRC64;

Query Match 50.6%; Score 41; DB 1; Length 311;
Best Local Similarity 66.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 LLAALGYKVRASD 15
   I IIIIII I
Db 90 LKALGYKVGKED 101

RESULT 6
MURC_AQUAE
ID MURC_AQUAE STANDARD; PRT; 454 AA.
AC O67373;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
DE ACETYLMURAMOYL-L-ALANINE SYNTHETASE).
GN MURC OR AQ1360.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- FUNCTION: CELL WALL FORMATION.
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE =
CC ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
CC -----

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DR EMBL; X52644; CAA36868.1; -;
 DR EMBL; X55034; CAA38868.1; -;
 DR EMBL; D10483; BAA01356.1; -;
 DR EMBL; AE000118; AAC73202.1; -;
 DR EMBL; U67892; AAB60787.1; -;
 DR PIR; JQ0545; CEECAM.

DR EcoGene; EG10619; murC.
 DR InterPro; IPR000713; Mur_ligase.
 DR Pfam; PF01225; Mur_ligase; 1.
 KW Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
 KW ATP-binding; Complete proteome.
 FT NP_BIND 126 132 ATP (POTENTIAL).
 FT MUTAGEN 344 344 G->D: IN MURC3.
 SQ SEQUENCE 491 AA; 53626 MW; D201B35931C013FB CRC64;

Query Match 50.6%; Score 41; DB 1; Length 491;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 ELIAALGYKVRSDMA 17
 Db 37 EVLANEGYQISGSDLA 52

RESULT 9
 ID YAO8_SCHPO STANDARD; PRT; 550 AA.
 AC Q10087;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PUTATIVE AMINO-ACID PERMEASE CLD3.08C.
 GN SPAC11D3.08C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.

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DR EMBL; Z68166; CAA92309.1; -;
 DR InterPro; IPR002293; AA_rel_permease.1.
 DR InterPro; IPR002027; Amino_acid_permease.
 DR Pfam; PF00324; aa_permeases; 1.
 DR PROSITE; PS00218; AMINO-ACID_PERMEASE_1; 1.
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 78 98 POTENTIAL.
 FT TRANSMEM 127 147 POTENTIAL.

FT TRANSMEM 177 197 POTENTIAL.
 FT TRANSMEM 201 221 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 283 303 POTENTIAL.
 FT TRANSMEM 336 356 POTENTIAL.
 FT TRANSMEM 386 406 POTENTIAL.
 FT TRANSMEM 411 431 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 FT TRANSMEM 481 501 POTENTIAL.
 SQ SEQUENCE 550 AA; 59918 MW; 3DD1EF6003896EAC CRC64;

Query Match 50.6%; Score 41; DB 1; Length 550;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYK 10
 Db 32 DELLMSLGYK 41

RESULT 10
 ID IF2P_YEAST STANDARD; PRT; 1002 AA.
 AC P39730;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE TRANSLATION INITIATION FACTOR IF-2.
 GN YAL035W OR FUN12.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=95249563; PubMed=7731988;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.;
 RT "The nucleotide sequence of chromosome I from Saccharomyces
 RT cerevisiae";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94357438; PubMed=8076820;
 RA Suttrave P., Shafer B.K., Strathern J.N., Hughes S.H.;
 RT "Isolation, identification and characterization of the FUN12 gene of
 RT Saccharomyces cerevisiae";
 RL Gene 146:209-213(1994).
 RN [3]
 RP REVISIONS.
 RC STRAIN=S288C / AB972;
 RA Vo D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

CC CHARACTERIZATION.
 RX MEDLINE=98288357; PubMed=9624054;
 RA Choi S.K., Lee J.H., Zoll W.L., Merrick W.C., Dever T.E.;
 RT "Promotion of met-tRNA^{Met} binding to ribosomes by yif2, a bacterial
 RT IF2 homolog in yeast";
 RL Science 280:1757-1760(1998).
 CC -1- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING
 CC THE BINDING OF THE FORMYL METHIONINE-TRNA TO RIBOSOMES. SEEMS TO
 CC FUNCTION ALONG WITH EIF-2.
 CC -1- SIMILARITY: BELONGS TO THE IF-2 FAMILY.

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Db 61 LAAGNWNVDSDLA 74

RESULT 13
VORR_PVRFU
ID VORR_PVRFU STANDARD; PRT; 311 AA.
AC Q51802;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORR (EC 1.-.-.-) (VOR) (2-
DE OXISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXISOVALERATE-
DE FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT).
VORR.
OS Pyrococcus furiosus.
GN Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-7.
RC STRAIN=DSM 3638;
RX MEDLINE=96125254; PubMed=8550425;
RA Kletzin A., Adams M.W.A.;
RT "Molecular and phylogenetic characterization of pyruvate and 2-
RT ketoisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus
RT and pyruvate ferredoxin oxidoreductase from Thermotoga maritima";
RL J. Bacteriol. 178:248-257(1996).
CC -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
KW EMBL; X85250; CAA59503.1; -.
KW Oxidoreductase.
SQ SEQUENCE 311 AA; 34766 MW; 07CC02452E3C6074 CRC64;

Query Match 48.1%; Score 39; DB 1; Length 311;
Best Local Similarity 58.3%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LAALGYKVRASD 15
| : : : : :
Db 90 LKAMGYKVKGED 101

RESULT 14
POTA_ECOLI
ID POTA_ECOLI STANDARD; PRT; 378 AA.
AC P23858;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
GN POTA OR B1126 OR K1831 OR ECS1571.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=92041956; PubMed=1939142;
RA Furuchi T., Kashiwagi K., Kobayashi H., Igarashi K.;
RT "Characteristics of the gene for a spermidine and putrescine
RT transport system that maps at 15 min on the Escherichia coli
RT chromosome.";
J. Biol. Chem. 266:20928-20933(1991).
[2]
SEQUENCE FROM N.A.
RN STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
[3]
SEQUENCE FROM N.A.
RN STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
[4]
SEQUENCE FROM N.A.
RN STRAIN=0157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
[5]
SEQUENCE FROM N.A.
RN STRAIN=0157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR SPERMIDINE/PUTRESCINE. PROBABLY RESPONSIBLE FOR ENERGY
CC COUPLING TO THE TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED.
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M64519; AAC37038.1; -.
DR EMBL; AE000212; AAC74210.1; -.
DR EMBL; D90747; BAA35946.1; -.
DR EMBL; D90748; BAA35948.1; -.
DR EMBL; AE005326; AAG55930.1; -.
DR EMBL; AP002555; BAB34994.1; -.
DR PIR; A40840; A40840.
DR Ecogene; EG10749; potA.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001687; ATP_GTP_A.

DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Transport; ATP-binding; Inner membrane; Complete proteome.
FT NP_BIND 50 57 ATP (BY SIMILARITY).
SQ SEQUENCE 378 AA; 43028 MW; 14DCA99329A344F3 CRC64;

Query Match 48.1%; Score 39; DB 1; Length 378;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DELLAALGYKVR 12
||| |||
DB 172 DESLSALDYKLR 183

RESULT 15

POTA_HAEIN STANDARD; PRT; 381 AA.
AC P45171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
GN POTA OR H11347
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerkavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInnes K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).

CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
CC FOR SPERMIDINE/PUTRESCINE. PROBABLY RESPONSIBLE FOR ENERGY
CC COUPLING TO THE TRANSPORT SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
CC -----
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DR EMBL; U32813; AAC22991.1; -;
DR TIGR; H11347; -;
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001687; ATP_GTP_A.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW Transport; ATP-binding; Inner membrane; Complete proteome.
FT NP_BIND 52 59 ATP (POTENTIAL).
SQ SEQUENCE 381 AA; 43429 MW; 3E61DD3D062EBE6A CRC64;

Query Match 48.1%; Score 39; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 DELLAALGYKVR 12
||| |||
DB 174 DESLSALDYKLR 185

Search completed: December 19, 2001, 17:10:29
Job time: 175 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 19, 2001, 17:07:14 ; Search time 22.97 Seconds
(without alignments)
108.256 Million cell updates/sec

Title: US-09-485-529-104
Perfect score: 81
Sequence: 1 DELLAALGYKVRASDMA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	623	10 Q9ST59	Q9ST59 triticum ae
2	78	96.3	625	10 Q9MB96	Q9MB96 oryza sativ
3	78	96.3	630	10 Q9ST48	Q9ST48 zea mays (m
4	70	86.4	511	10 Q9C8Y3	Q9C8Y3 arabidopsis
5	70	86.4	523	10 Q9LF53	Q9LF53 arabidopsis
6	70	86.4	532	10 Q23643	Q23643 arabidopsis
7	70	86.4	532	10 Q23724	Q23724 arabidopsis
8	70	86.4	533	10 Q9LQT8	Q9LQT8 arabidopsis
9	70	86.4	547	10 Q9SRP9	Q9SRP9 arabidopsis
10	70	86.4	587	10 Q23725	Q23725 arabidopsis
11	70	86.4	587	10 Q23642	Q23642 arabidopsis
12	70	86.4	587	10 Q9SLH3	Q9SLH3 arabidopsis
13	70	86.4	662	10 Q65367	Q65367 arabidopsis
14	44	54.3	411	4 Q43916	Q43916 homo sapien
15	44	54.3	466	2 Q45645	Q45645 bacillus su
16	44	54.3	466	2 Q34666	Q34666 bacillus su
17	44	54.3	1149	12 Q9WBQ8	Q9WBQ8 porcine rep
18	44	54.3	1457	12 Q9WJB3	Q9WJB3 porcine rep
19	44	54.3	1457	12 Q9WBQ4	Q9WBQ4 porcine rep

20	44	54.3	1457	12 Q9DY97	Q9DY97 porcine rep
21	44	54.3	1463	12 Q9YN01	Q9YN01 porcine rep
22	44	54.3	1463	12 Q9J7C0	Q9J7C0 porcine rep
23	44	54.3	1463	12 Q9ENK5	Q9ENK5 porcine rep
24	44	54.3	1463	12 Q9E8M9	Q9E8M9 porcine rep
25	44	54.3	1463	12 Q99BU5	Q99BU5 porcine rep
26	44	54.3	1463	12 Q99AV5	Q99AV5 porcine rep
27	44	54.3	3956	12 Q9DLN9	Q9DLN9 porcine rep
28	44	54.3	3960	12 Q9DLP1	Q9DLP1 porcine rep
29	44	54.3	3960	12 Q9DLP0	Q9DLP0 porcine rep
30	44	54.3	3960	12 Q9DLN8	Q9DLN8 porcine rep
31	42	51.9	263	10 Q80476	Q80476 arabidopsis
32	42	51.9	516	10 Q9SAI7	Q9SAI7 arabidopsis
33	41	50.6	217	2 P70930	P70930 borrelia mi
34	41	50.6	272	1 Q9YAH8	Q9YAH8 aeropyrum p
35	41	50.6	463	2 Q9JWD2	Q9JWD2 neisseria m
36	41	50.6	467	2 Q30707	Q30707 streptomyce
37	41	50.6	469	2 Q9K0Y1	Q9K0Y1 neisseria m
38	41	50.6	506	2 Q9JSZ8	Q9JSZ8 neisseria m
39	41	50.6	999	12 P91577	P91577 choristoneu
40	41	50.6	1411	12 Q06503	Q06503 lactate deh
41	40	49.4	96	2 Q916C5	Q916C5 pseudomonas
42	40	49.4	330	2 Q912R2	Q912R2 pseudomonas
43	40	49.4	477	2 Q9PF80	Q9PF80 xylella fas
44	40	49.4	480	2 Q9HW02	Q9HW02 pseudomonas
45	40	49.4	487	2 Q9GRG6	Q9GRG6 pseudomonas

ALIGNMENTS

RESULT 1					
Q9ST59					
ID Q9ST59	PRELIMINARY;	PRT;	623 AA;		
AC Q9ST59					
DT 01-MAY-2000	(TReMBLrel. 13, Created)				
DT 01-MAY-2000	(TReMBLrel. 13, Last sequence update)				
DT 01-JUN-2001	(TReMBLrel. 17, Last annotation update)				
DE GIBBERELLIN RESPONSE MODULATOR.					
GN RHT-DIA.					
OS Triticum aestivum (Wheat).					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;					
OC Triticeae; Triticum.					
OX NCBI_TaxID=4565;					
RP [1]					
RN SEQUENCE FROM N.A.					
RA MEDLINE=99347734; PubMed=10421366;					
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,					
RA Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,					
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;					
RT "Green revolution" genes encode mutant gibberellin response					
RT modulators.;					
RL Nature 400:256-261(1999).					
DR EMBL; AJ242531; CAB51555.1; .					
SQ SEQUENCE 623 AA; 65337 MW; F2BAC34996D0A84F CRC64;					

Query Match 100.0%; Score 81; DB 10; Length 623;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1	DELLAALGYKVRASDMA 17
Db 38	DELLAALGYKVRASDMA 54

RESULT 2					
Q9MB96					
ID Q9MB96	PRELIMINARY;	PRT;	625 AA.		
AC Q9MB96					
DT 01-OCT-2000	(TReMBLrel. 15, Created)				
DT 01-OCT-2000	(TReMBLrel. 15, Last sequence update)				

DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE OSGAI.
GN OSGAI.

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RX MEDLINE=20179680; PubMed=10713441;
RA Ogawa M., Kusano T., Katsumi M., Sano H.;
RT "Rice gibberellin-insensitive gene homolog, OSGAI, encodes a nuclear-
RT localized protein capable of gene activation at transcriptional
RT level".
RL Gene 245:21-29(2000).
DR EMBL; AB030956; BAA90749.1; -.
SQ SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;

Query Match 96.3%; Score 78; DB 10; Length 625;
Best Local Similarity 94.1%; Pred. No. 7.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DELLAALGYKVRSDMA 17
DB 39 DELLAALGYKVRSDMA 55

RESULT 3

Q9ST48 PRELIMINARY; PRT; 630 AA.

AC Q9ST48;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).
GN D8.

OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=99347734; PubMed=10421366;
RA Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
RA Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,
RA Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P.;
RT "Green revolution" genes encode mutant gibberellin response
RT modulators".
RL Nature 400:256-261(1999).
DR EMBL; AJ242530; CAB51557.1; -.
FT NON_TER 630
SQ SEQUENCE 630 AA; 66028 MW; 3D56851726C51042 CRC64;

Query Match 96.3%; Score 78; DB 10; Length 630;
Best Local Similarity 94.1%; Pred. No. 7.3e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DELLAALGYKVRSDMA 17
DB 38 DELLAALGYKVRSDMA 54

RESULT 4

Q9C8Y3 PRELIMINARY; PRT; 511 AA.

AC Q9C8Y3;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE GIBBERELLIN REGULATORY PROTEIN, PUTATIVE.
GN T27F4.10.

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana".
RL Nature 408:816-820(2000).
DR EMBL; AC020665; AAG52171.1; -.
SQ SEQUENCE 511 AA; 56754 MW; 1560071697C92A9F CRC64;

Query Match 86.4%; Score 70; DB 10; Length 511;
Best Local Similarity 82.4%; Pred. No. 0.0013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DELLAALGYKVRSDMA 17
DB 32 DELLVVLGYKVRSDMA 48

RESULT 5

Q9LF53 PRELIMINARY; PRT; 523 AA.

AC Q9LF53;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE RGA-LIKE PROTEIN.
GN K3M16_60.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL391150; CAC01893.1; -.
SQ SEQUENCE 523 AA; 57326 MW; 0F6CE0BD13403C35 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 523;
Best Local Similarity 82.4%; Pred. No. 0.0014;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
 ||||| |||||:||||
 Db 34 DELAVLGYKVRSSDMA 50

RESULT 6
 O23643 PRELIMINARY; PRT; 532 AA.
 AC O23643;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE RGA2 PROTEIN.
 GN RGA2

OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97379310; PubMed=9237632;
 RA Truong H.N., Caboche M., Daniel-Vedele F.;
 RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
 RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
 RL FEBS Lett. 410:213-218(1997).
 DR EMBL; Y11337; CAA72178.1; -;
 DR Mendel; 24146; Arath:3051;24146.
 SQ SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 532;
 Best Local Similarity 82.4%; Pred. No. 0.0014;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
 ||||| |||||:||||
 Db 27 DELAVLGYKVRSSDMA 43

RESULT 7
 O23724 PRELIMINARY; PRT; 532 AA.
 AC O23724;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE GAI PROTEIN.
 GN GAI

OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LANDSBERG ERECTA;
 RX MEDLINE=98051192; PubMed=9389651;
 RA Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,
 RA Murphy G.P., Harberd N.P.;
 RT "The Arabidopsis GAI gene defines a signaling pathway that negatively
 RT regulates gibberellin responses.";
 RL Genes Dev. 11:3194-3205(1997).
 DR EMBL; Y15193; CAA75492.1; -;
 DR Mendel; 24070; Arath:3051;24070.
 SQ SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 532;
 Best Local Similarity 82.4%; Pred. No. 0.0014;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
 ||||| |||||:||||
 Db 27 DELAVLGYKVRSSDMA 43

RESULT 8
 Q9LQ78 PRELIMINARY; PRT; 533 AA.
 AC Q9LQ78;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE F10B6.34.

OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
 RA Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
 RA Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
 RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
 RA Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
 RT I.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chlou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu S., Liu J., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC006917; AAF79228.1; -;

SQ SEQUENCE 533 AA; 58926 MW; 6464B8C129D79528 CRC64;
 Query Match 86.4%; Score 70; DB 10; Length 533;
 Best Local Similarity 82.4%; Pred. No. 0.0014;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17
 ||||| |||||:||||
 Db 28 DELAVLGYKVRSSDMA 44

RESULT 9
 Q9SRP9 PRELIMINARY; PRT; 547 AA.
 AC Q9SRP9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RGA1-LIKE PROTEIN.
 GN T2IP5.13.

OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC009895; AAF01590.1; --
SQ SEQUENCE 547 AA; 60493 MW; C4D18D5951D95634 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 547;
Best Local Similarity 82.4%; Pred. No. 0.0014;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGYKVRASDMA 17
Db 44 DELLAVLGYKVRSEMA 60

RESULT 10
ID O23725 PRELIMINARY; PRT; 587 AA.
AC O23725;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE GRS PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Peng J., Carol P., Richards D.E., King K.E., Cowling R.J.,
RA Murphy G.P., Harberd N.P.;
RL Genes Dev. 0:0-0(0)
DR EMBL: Y15194; CAA75493.1; --
DR Mendel: 24071; Arath;3051;24071.
SQ SEQUENCE 587 AA; 64006 MW; F6F6C7738EE7DCA9 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 587;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGYKVRASDMA 17
Db 44 DELLAVLGYKVRSEMA 60

RESULT 11
ID O23642 PRELIMINARY; PRT; 587 AA.
AC O23642;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE RGAL PROTEIN.
GN RGAL.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97379310; PubMed=9237632;
RA Truong H.N., Caboche M., Daniel-Vedele F.;

RT "Sequence and characterization of two Arabidopsis thaliana cDNAs
RT isolated by functional complementation of a yeast gln3 gdh1 mutant.";
RL FEBS Lett. 410:213-218(1997).
DR EMBL: Y11336; CAA72177.1; --
DR Mendel: 24145; Arath;3051;24145.
SQ SEQUENCE 587 AA; 64023 MW; DOA7A3C741FB51EF CRC64;

Query Match 86.4%; Score 70; DB 10; Length 587;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGYKVRASDMA 17
Db 44 DELLAVLGYKVRSEMA 60

RESULT 12
ID O9SLH3 PRELIMINARY; PRT; 587 AA.
AC O9SLH3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PUTATIVE RGAL, GIBERELLIN RESPONSE MODULATION PROTEIN.
GN AT2G01570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell L.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RL Nature 402:761-768(1999).
DR EMBL: AC005560; AAC67333.1; --
SQ SEQUENCE 587 AA; 64035 MW; FC92E7F9408072AA CRC64;

Query Match 86.4%; Score 70; DB 10; Length 587;
Best Local Similarity 82.4%; Pred. No. 0.0015;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DELLAALGYKVRASDMA 17
Db 44 DELLAVLGYKVRSEMA 60

RESULT 13
ID O65367 PRELIMINARY; PRT; 662 AA.
AC O65367;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RGAL PROTEIN.
GN RGA-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=CV. COL-0;
RA Sanchez-Fernandez R., Ardiiles-Diaz W., van Montagu M., Inze D.,
RA May M.J.;
RT "Cloning of the Arabidopsis thaliana RGA-like gene, a putative member
of the VHIID domain transcription factor family";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ224957; CAA12242.1; -;
DR Mendel; 29006; Arath;3051;29006.

DR InterPro; IPR001680; WD40.

DR Pfam; PF00400; WD40; 1.

DR SMART; SM00320; WD40; 1.

DR PROSITE; PS50082; WD-REPEATS_2; 1.

DR PROSITE; PS50294; WD-REPEATS_REGION; 1.

DR Repeat; WD repeat.

KW SEQUENCE 662 AA; 73126 MW; 958AB73D42121CA8 CRC64;

Query Match 86.4%; Score 70; DB 10; Length 662;

Best Local Similarity 82.4%; Pred. No. 0.0018;

Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DELLAALGYKVRASDMA 17

DB 183 DELLVVLGYKVRSSDMA 199

RESULT 14

ID O43916 PRELIMINARY; PRT; 411 AA.

AC O43916;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)

DE CHONDROITIN-6-SULFOTRANSFERASE.

GN CHST1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97189336; PubMed=9117134;

RA Williams K.J.;

RT "Atherosclerosis: cell biology and lipoproteins.";

RL Curr. Opin. Lipidol. 7:0-0(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Peng T., Tabas I., Williams K.J.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE=98070405; PubMed=9405439;

RA Fukuta M., Inazawa J., Torii T., Tsuzuki K., Shimada E., Habuchi O.;

RT "Molecular cloning and characterization of human keratan sulfate

Gal-6-sulfotransferase.";

RL J. Biol. Chem. 272:32321-32328(1997).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=UMBILICAL VEIN ENDOTHELIUM;

RX MEDLINE=99168906; PubMed=10049591;

RA Li X., Tedder T.F.;

RT "CHST1 and CHST2 sulfotransferases expressed by human vascular

endothelial cells: cDNA cloning, expression, and chromosomal

localization.";

RL Genomics 55:345-347(1999).

DR EMBL; U65637; AAC28776.1; -;

DR EMBL; AB003791; BAA24840.1; -;

DR EMBL; AF090137; AAD19878.1; -;

DR Transference.

KW SEQUENCE 411 AA; 46714 MW; F07D0A23B6338A09 CRC64;

Query Match 54.3%; Score 44; DB 4; Length 411;

Best Local Similarity 57.1%; Pred. No. 27;

Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ELLAALGYKVRASD 15

DB 378 QVLAQLGYKIAASE 391

RESULT 15

Q45645

ID Q45645 PRELIMINARY; PRT; 466 AA.

AC Q45645;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ORF01 DNA.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PY17;

RX MEDLINE=97149292; PubMed=8996100;

RA Marasco R., Varcamonti M., Ricca E., Sacco M.;

RT "A new Bacillus subtilis gene with homology to Escherichia coli prc.";

RL Gene 183:149-152(1996).

DR EMBL; X98341; CAA66987.1; -;

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR003581; TSpc.

DR Pfam; PF00595; PDZ; 1.

DR PROSITE; PS50106; PDZ; 1.

DR SMART; SM00228; PDZ; 1.

DR SMART; SM00245; TSpc; 1.

SQ SEQUENCE 466 AA; 51413 MW; 4430B459C45E8714 CRC64;

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0; 0; 0; 0; 0;

Search completed: December 19, 2001, 17:10:13

Job time: 179 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 17:30:48 ; Search time 1422.71 Seconds
(without alignments)
591.376 Million cell updates/sec

Title: US-09-485-529-105

Perfect score: 51

Sequence: 1 gacgagctgctggcgcgct.....tcgcggctccgacatggcg 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba:*
- 2: gb_hgt:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_om:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pi:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htgo_hum:*
- 31: em_htgo_inv:*
- 32: em_htgo_rod:*
- 33: em_htg_hum:*
- 34: em_htg_inv:*
- 35: em_htg_rod:*
- 36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*

Result No.	Score	Query Match	Length	DB	ID	Description	
1	51	100.0	51	6	AX005896	AX005896 Sequence	
2	51	100.0	453	6	AX005857	AX005857 Sequence	
3	51	100.0	1872	8	TAE242531	AJ242531 Triticum	
4	51	100.0	2125	6	AX005805	AX005805 Sequence	
5	51	100.0	2709	6	AX005794	AX005794 Sequence	
c	49	96.1	324	6	AX005867	AX005867 Sequence	
	7	45.2	88.6	770	6	AX005803	AX005803 Sequence
8	45.2	88.6	2500	8	AB030956	AB030956 Oryza sat	
9	45.2	88.6	122497	8	AC087797	AC087797 Oryza sat	
10	44.2	86.7	725	6	AX005810	AX005810 Sequence	
11	43.2	84.7	200	6	AX005860	AX005860 Sequence	
12	39.8	78.0	302	6	AX005807	AX005807 Sequence	
13	39.8	78.0	371	6	AX005808	AX005808 Sequence	
14	39.8	78.0	1890	8	ZMA242530	AJ242530 Zea mays	
15	39.8	78.0	2255	6	AX005806	AX005806 Sequence	
16	39	76.5	416	6	AX005809	AX005809 Sequence	
17	29.8	58.4	1542	1	AF071051	AF071051 Streptomyces	
18	29.8	58.4	1542	6	AR151707	AR151707 Sequence	
19	29.8	58.4	1542	6	AX006515	AX006515 Sequence	
20	29.8	58.4	6584	1	SCPACAS	X84101 S.clavuliger	
21	29.8	58.4	11604	6	AR151704	AR151704 Sequence	
22	29.8	58.4	15079	6	AR151702	AR151702 Sequence	
23	29.8	58.4	15120	1	SCU87786	U87786 Streptomyces	
24	29.4	57.6	309	6	AX005855	AX005855 Sequence	
25	28.6	56.1	230	6	AX005861	AX005861 Sequence	
26	28.2	55.3	2295	1	STMTRIP	L27466 Streptomyces	
c	27	28.2	26555	1	SC2G1	AL391014 Streptomyces	
	28	27.8	54.5	1691	8	AB057426	AB057426 Coriolus
29	27.6	54.1	4081	8	ATA224957	AJ224957 Arabidopsis	
c	30	27.6	54.1	26604	8	ATK3M16	AL391150 Arabidopsis
	31	27.6	54.1	45335	1	SCC57A	AL136519 Streptomyces
32	27.6	54.1	82289	8	ATAC009895	AC009895 Arabidopsis	
33	27.6	54.1	85702	8	AC020665	AC020665 Arabidopsis	
34	27.6	54.1	132699	8	AC006917	AC006917 Genomic s	
c	35	27.4	53.7	285	6	AX005865	AX005865 Sequence
	36	27	52.9	4523	14	MMULGENES	X95710 Pseudorabies
c	37	26.6	52.2	345783	1	AP003001	AP003001 Mesorhizobium
	38	26	51.0	1951	8	ATRG42	Y11337 A.thaliana
39	26	51.0	1964	6	A64697	A64697 Sequence 1	
40	26	51.0	1964	8	ATY15193	Y15193 Arabidopsis	
c	41	26	51.0	11093	1	AE005134	AE005134 Halobacterium
	42	26	51.0	11925	1	AE005111	AE005111 Halobacterium
c	43	26	51.0	12510	1	AE005848	AE005848 Caulobacter
	44	26	51.0	33320	1	SC9B10	AL009204 Streptomyces
45	26	51.0	37000	14	BHTIUL	Z78205 Bovine herpes	

ALIGNMENTS

RESULT	1
AX005896	
LOCUS	Sequence 105 bp DNA
DEFINITION	Sequence 105 from Patent WO9909174.
ACCESSION	AX005896
VERSION	AX005896.1 GI:9928885
KEYWORDS	bread wheat.
SOURCE	Triticum aestivum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticeae; Triticum.
REFERENCE	1 (bases 1 to 51)
AUTHORS	Harberd,N.P. and Peng,J.
TITLE	Genetic control of plant growth and development
JOURNAL	Patent: WO 9909174-A 105 25-FEB-1999;
FEATURES	HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
source	Location/Qualifiers
	1..51
	/organism="Triticum aestivum"

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BASE COUNT      7 a      16 c      21 g      7 t
ORIGIN

Query Match      100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gacgagctgctggcgccgctcggtgacagtgccgctccgacatggcg 51
|||||
Db 1 GACGAGCTGCTGGCGCGCTCGGTGACAGGTGCGCGCTCCGACATGGCG 51

RESULT 2
LOCUS      AX005857      453 bp      DNA      PAT      24-AUG-2000
DEFINITION      Sequence 66 from Patent WO9909174;
ACCESSION      AX005857
VERSION      AX005857.1 GI:9928852
KEYWORDS      bread wheat.
SOURCE      Triticum aestivum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE      1 (bases 1 to 453)
AUTHORS      Harberd,N.P. and Peng,J.
TITLE      Genetic control of plant growth and development
JOURNAL      Patent: WO 9909174-A 66 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
FEATURES      source
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Best Local Similarity 100.0%; Pred. No. 7.8e-05;
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Db 273 GACGAGCTGCTGGCGCGCTCGGTGACAGGTGCGCGCTCCGACATGGCG 323

RESULT 3
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DEFINITION      Triticum aestivum rht-Dla gene for gibberellin response modulator.
ACCESSION      AJ242531
VERSION      AJ242531.1 GI:5640156
KEYWORDS      gibberellin response modulator; rht-Dla gene.
SOURCE      bread wheat.
ORGANISM      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Pooideae; Triticeae; Triticum.
1 (bases 1 to 1872)
Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M.,
Flintham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pellica,F.,
Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P.
'Green revolution' genes encode mutant gibberellin response
modulators
Nature 400 (6741), 256-261 (1999)
99347734
2 (bases 1 to 1872)
Harberd,N.P., Peng,J. and Richards,D.E.
Green revolution genes encode mutant gibberellin response
modulators
Unpublished
3 (bases 1 to 1872)
Richards,D.E.
Direct Submission
Submitted (25-MAY-1999) Richards D.E., Molecular Genetics, John
Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
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ORIGIN

Query Match      100.0%; Score 51; DB 8; Length 1872;
Best Local Similarity 100.0%; Pred. No. 5e-05;
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RESULT 4
LOCUS      AX005805      2125 bp      DNA      PAT      24-AUG-2000
DEFINITION      Sequence 14 from Patent WO9909174.
ACCESSION      AX005805
VERSION      AX005805.1 GI:9928802
KEYWORDS      bread wheat.
SOURCE      Triticum aestivum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
REFERENCE      1 (bases 1 to 2125)
AUTHORS      Harberd,N.P. and Peng,J.
TITLE      Genetic control of plant growth and development
JOURNAL      Patent: WO 9909174-A 14 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

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Query Match	96.1%	Score 49;	DB 6;	Length 324;
Best Local Similarity	96.1%	Pred. No. 0.00032.		

BAC clone OSJNBb0022E02 is from *Oryza sativa* chromosome 3
 The orientation of the sequence is from SP6 to T7 end of the BAC clone.
 Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (<http://www.softberry.com/>), genscan and Genscan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCan.html>), GeneMarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/GeneMark/>), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact.mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shtml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Arian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

FEATURES

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CDS

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 20:52:13 ; Search time 142.61 seconds
(without alignments)
306.596 Million cell updates/sec

Title: US-09-485-529-105

Perfect score: 51

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Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	51	100.0	453	20	AA36263 DNA sequence obtai
3	51	100.0	2125	20	AA36279 Wheat Rht clone 5a
4	51	100.0	2709	20	AA36275 Composite DNA sequ
5	49	96.1	324	20	AA36273 DNA sequence obtai
6	45.2	88.6	770	20	AA36277 Rice EST D39460 se
7	44.2	86.7	725	20	AA36276 Partial cDNA sequ
8	43.2	84.7	200	20	AA36266 DNA sequence obtai
9	39.8	78.0	302	20	AA36281 Partial sequence o
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41	23	45.1	632	22	AA36271	Murine Hoxcl3 prot
42	23	45.1	1458	19	AA36271	Keratan sulphate 6
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ALIGNMENTS

RESULT 1

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ID AAX36284 standard; DNA; 51 BP.

XX AC AAX36284;

XX DT 16-JUL-1999 (first entry)

XX DE Oligonucleotide derived from the wheat rht gene.

XX DE Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

XX OS Triticum aestivum.

XX PN WO9909174-A1.

XX PD 25-FEB-1999.

XX PF 07-AUG-1998; 98WO-GB02383.

XX PR 13-AUG-1997; 97GB-0017192.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Harberd NP, Peng J, Richards DE;

XX DR WPI; 1999-181040/15.

XX PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Claim 3; Page 53; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is
CC derived from the wheat rht gene.

SQ Sequence 51 BP; 7 A; 16 C; 21 G; 7 T; 0 other;

Query Match 100.0%; Score 51; DB 20; Length 51;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatggcg 51

RESULT 2

AAAX36263
ID AAX36263 standard; DNA; 453 BP.

XX AAX36263;

DT 16-JUL-1999 (first entry)

XX DNA sequence obtained after sequencing wheat Rht clone 14a1.

XX Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

XX *Triticum aestivum*.

OS WO9909174-A1.

XX 25-FEB-1999.

XX 07-AUG-1998; 98WO-GB02383.

XX 13-AUG-1997; 97GB-0017192.

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX Harberd NP, Peng J, Richards DE;

XX WPI; 1999-181040/15.

XX New *Triticum aestivum* polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 2b(9); 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants

CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence was
CC obtained after partially sequencing wheat Rht clone 14a1.

XX SQ Sequence 453 BP; 85 A; 136 C; 158 G; 67 T; 7 other;

Query Match 100.0%; Score 51; DB 20; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.2e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 273 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatggcg 323

RESULT 3

AAAX36279

ID AAX36279 standard; DNA; 2125 BP.

XX AAX36279;

XX 16-JUL-1999 (first entry)

XX Wheat Rht clone 5a1 genomic sequence.

XX Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;

KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

XX *Triticum aestivum*.

XX WO9909174-A1.

XX 25-FEB-1999.

XX 07-AUG-1998; 98WO-GB02383.

XX 13-AUG-1997; 97GB-0017192.

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX Harberd NP, Peng J, Richards DE;

XX WPI; 1999-181040/15.

XX P-PSDB; AAY02540.

XX New *Triticum aestivum* polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

XX Disclosure; Fig 8a; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the wheat Rht clone 5a1 genomic sequence.

XX SQ Sequence 2125 BP; 325 A; 768 C; 723 G; 309 T; 0 other;

Query Match 100.0%; Score 51; DB 20; Length 2125;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gacgagctgctggcgcgctcggtacaagtgcgcgctccgacatggcg 51
|||||
Db 139 gacgagctgctggcgcgctcggtacaagtgcgcgctccgacatggcg 189
|||||

RESULT 4
AA36275
ID AAX36275 standard; DNA; 2709 BP.
XX
AC AAX36275;
XX
DT 16-JUL-1999 (first entry)
XX
DE Composite DNA sequence of wheat Rht gene.
XX
DE Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.
XX
OS Triticum aestivum.
XX
PN WO9909174-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
DR WPI; 1999-181040/15.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 3a; 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the composite DNA sequence of wheat Rht gene.
XX
SQ Sequence 2709 BP; 473 A; 900 C; 823 G; 482 T; 31 other;

Query Match 100.0%; Score 51; DB 20; Length 2709;
Best Local Similarity 100.0%; Pred. No. 6.5e-08;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gacgagctgctggcgcgctcggtacaagtgcgcgctccgacatggcg 51
|||||
Db 273 gacgagctgctggcgcgctcggtacaagtgcgcgctccgacatggcg 323
|||||

RESULT 5

AA36273/C
ID AAX36273 standard; DNA; 324 BP.
XX

AC AAX36273;

XX 16-JUL-1999 (first entry)

XX DNA sequence obtained after sequencing wheat Rht clone 5a1.

XX Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

XX Triticum aestivum.

XX WO9909174-A1.

XX 25-FEB-1999.

XX 07-AUG-1998; 98WO-GB02383.

XX 13-AUG-1997; 97GB-0017192.

XX (PLAN-) PLANT BIOSCIENCE LTD.

XX Harberd NP, Peng J, Richards DE;

XX WPI; 1999-181040/15.

XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 2c(6); 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence was
CC obtained after partially sequencing wheat Rht clone 5a1.

XX Sequence 324 BP; 39 A; 141 C; 85 G; 56 T; 3 other;

Query Match 96.1%; Score 49; DB 20; Length 324;
Best Local Similarity 96.1%; Pred. No. 2.7e-07;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gacgagctgctggcgcgctcggtacaagtgcgcgctccgacatggcg 51
|||||
Db 162 GNCNGCTGCTGGCGGCGCTCGGGTACAAAGGTGGCGGCTCGGCGGCG 112
|||||

RESULT 6

AA36277
ID AAX36277 standard; DNA; 770 BP.
XX

AC AAX36277;

XX 16-JUL-1999 (first entry)

XX Rice EST D39460 sequence, homologous to wheat Rht gene.
DE
XX

AAZ60717
ID AAZ60717 standard; DNA; 1542 BP.
AC
XX
AC AAZ60717;
XX
XX
DT 16-MAY-2000 (first entry)
DE
DE DNA encoding a beta-lactam synthetase enzyme.
XX
XX Beta-lactam synthetase; orf3; clavulanic acid biosynthesis cluster;
KW beta-amino acid; beta-lactam; clavulanic acid biosynthesis;
KW N-substituted azetidinone; clavulanic acid; beta-lactamase inhibitor;
KW (2S)-5-guanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid;
KW beta-lactam antibiotic; infection; clavulams; ss.
XX
OS Streptomyces clavuligerus.
XX
FH Key Location/Qualifiers
FT CDS 4..1542
FT /*tag= a
XX
XX WO200003581-A1.
XX
XX 27-JAN-2000.
PD
XX
XX 15-JUL-1999; 99WO-GB02301.
PF
XX
XX 17-JUL-1998; 98GB-0015666.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA
XX
XX Barton B, McNaughton HJ, Schofield CJ, Thirkettle JE;
PI
XX
XX WPI; 2000-182296/16.
DR
DR P-PSDB; AAY68875.
XX
XX Preparation of N-substituted azetidinone, useful as intermediate for
PT clavulanic acid, by cyclisation of N-substituted aminopropanoic acid in
PT presence of beta-lactam synthetase
XX
XX Claim 8; Page 22; 3lpp; English.
XX
XX The present sequence encodes a beta-lactam synthetase polypeptide.
CC The enzyme is encoded by orf3 of the clavulanic acid biosynthesis
CC cluster. This enzyme converts a beta-amino acid (formed from arginine
CC and pyruvate) into the beta-lactam form, early in the clavulanic acid
CC biosynthesis pathway. The beta-lactam synthetase enzyme is used for
CC the preparation of N-substituted azetidinones from N-substituted
CC 2-aminopropanoic acid derivatives. The method is particularly used
CC to make (2S)-5-guanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid from
CC N2-(2-carboxyethyl)-(S)-arginine. (2S)-5-guanidino-2-(2-oxo-azetidin-
CC 1-yl)pentanoic acid is an intermediate for clavulanic acid, a known
CC inhibitor of beta-lactamase, used in combination with beta-lactam
CC antibiotics for treatment of infections. More generally,
CC N-substituted azetidinones are intermediates for other clavulams and
CC their derivatives.
XX
XX Sequence 1542 BP; 190 A; 591 C; 557 G; 204 T; 0 other;

Query Match 58.4%; Score 29.8; DB 21; Length 1542;
Best Local Similarity 75.5%; Pred. No. 0.43;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 cgagctgctggcggcgctgggtacaggtgcgcgcctccgacatggcg 51
|||||
Db 909 cgagctgctggcgcagctcccgtagcggtgtggcctccgagtcggtg 957
|||||

RESULT 14
ID AAZ60717
XX AAZ60717 standard; DNA; 15079 BP.

AC AAQ91580;
XX
XX 13-NOV-1995 (first entry)
DE
DE S. clavuligerus cla gene region.
XX
XX Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
KW cla gene; ds.
XX
XX Streptomyces clavuligerus.
OS
XX
FH Key Location/Qualifiers
FT CDS complement (49..1745)
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FT /label= ORF1
FT 2216..3937
FT /*tag= b
FT /label= ORF2
FT 3940..5481
FT /*tag= c
FT /label= ORF3
FT 5654..6595
FT /*tag= d
FT /label= ORF4
FT /note= "cla gene"
FT 6611..7588
FT /*tag= e
FT /label= ORF5
FT 7895..9076
FT /*tag= f
FT /label= ORF6
FT 9241..10908
FT /*tag= g
FT /label= ORF7
FT complement (10998..12296)
FT /*tag= h
FT /label= ORF8
FT complement (12662..13365)
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FT /label= ORF9
FT 13769..14995
FT /*tag= j
FT /label= ORF10
XX
XX CA2108113-A.
PN
XX
XX 09-APR-1995.
PD
XX
XX 08-OCT-1993; 93CA-2108113.
PF
XX
XX 08-OCT-1993; 93CA-2108113.
PR
XX
XX (UYAL-) UNIV ALBERTA.
PA
XX
XX Aldoo KA, Jensen SE, Paradkar AS;
PI
XX
XX WPI; 1995-207301/28.
DR
DR P-PSDB; AAR77858; AAR77859; AAR77860; AAR77861; AAR77862; AAR77863;
DR AAR77864; AAR77865; AAR77866; AAR77867.
XX
XX Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for
PT biosynthesis of the antibiotic in Streptomyces hosts which do not
PT naturally produce clavulanate
XX
XX Disclosure; Fig.2; 4lpp; English.
PS
XX
XX A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22
CC kb) constructed in cosmid pLAFR3 was screened for the cla gene using
CC a probe based on a partial N-terminal sequence from the CLA enzyme.
CC Isolated clone K6L1 included a 15kb fragment having the sequence
CC given in AAQ91580 that included the cla gene (ORF4).
XX
XX Sequence 15079 BP; 2097 A; 5488 C; 5324 G; 2170 T; 0 other;

Search completed: December 19, 2001, 22:25:14
Job time: 5581 sec

Query Match 58.4%; Score 29.8; DB 16; Length 15079;
Best Local Similarity 75.5%; Pred. No. 0.47;
Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 3 cgagctgtcggcggtcggtacaaagtcggtcgccctccgacatggcg 51
|||||
Db 4848 cgagctgtcggcggtcggtacaaagtcggtcgccctccgacatggcg 4896
|||||

RESULT 15
AAX36261
ID AAX36261 standard; DNA; 309 BP.
XX
AC AAX36261;
XX
DT 16-JUL-1999 (first entry)
XX
DE DNA sequence obtained after sequencing wheat Rht clone 14a1.
XX
KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.
XX
OS Triticum aestivum.
XX
PN WO9909174-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
XX WPI; 1999-181040/15.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 2b(7); 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence was
CC obtained after partially sequencing wheat Rht clone 14a1.
XX
SQ Sequence 309 BP; 47 A; 102 C; 102 G; 45 T; 13 other;

Query Match 57.6%; Score 29.4; DB 20; Length 309;
Best Local Similarity 93.8%; Pred. No. 0.55;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 20 tcgggtacaaagtcggtcggtcgccctccgacatggcg 51
|
Db 16 ttgggtacaaagtcggtcggtcgccctccgacatggcg 47
|

Best Local Similarity 94.0%; Pred. NO. 0.00071;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||
Db 97 GACGAGCTGCTGCGCGCTCGGTACAAAGGTGCGGTCTCGCATGCGC 146

RESULT 2

LOCUS C27475 388 bp mRNA EST 06-AUG-1997
DEFINITION C27475 Rice callus cDNA Oryza sativa cDNA clone C51976_1A, mRNA sequence.
ACCESSION C27475
VERSION C27475.1 GI:2311320
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 388)
Yamamoto, K. and Sasaki, T.
Rice cDNA from callus 1997
Unpublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/.

FEATURES
source
1..388
Location/Qualifiers
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="C51976_1A"
/clone_lib="Rice callus cDNA"
/tissue_type="callus"
/dev_stage="callus"
BASE COUNT 83 a 102 c 134 g 65 t 4 others
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/clone_lib="Rice callus cDNA"
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/dev_stage="callus"

Query Match 88.6%; Score 45.2; DB 11; Length 388;
Best Local Similarity 94.0%; Pred. No. 0.00072;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||
Db 271 GACGAGCTGCTGCGCGCTCGGTACAAAGGTGCGGTCTCGCATGCGC 320

RESULT 3

LOCUS AU091413 399 bp mRNA EST 05-JUN-2000
DEFINITION AU091413 Rice cDNA from immature leaf including apical meristem sequence.
ACCESSION AU091413
VERSION AU091413.1 GI:8251089
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 399)
Sasaki, T. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem (2000)
Unpublished (2000)
Contact: Takuji Sasaki

Query Match 88.6%; Score 45.2; DB 11; Length 388;
Best Local Similarity 94.0%; Pred. No. 0.00072;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||
Db 271 GACGAGCTGCTGCGCGCTCGGTACAAAGGTGCGGTCTCGCATGCGC 320

RESULT 4

LOCUS AU222715 467 bp mRNA EST 30-JUL-2001
DEFINITION AU222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence.
ACCESSION AU222715
VERSION AU222715.1 GI:15008327
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 467)
Sasaki, T. and Yamamoto, K.
Rice cDNA from etiolated shoot (2001)
Unpublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'

Query Match 88.6%; Score 45.2; DB 10; Length 467;
Best Local Similarity 94.0%; Pred. No. 0.00073;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||

National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'
E60220_1A.

FEATURES

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Location/Qualifiers
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/dev_stage="immature leaf including apical meristem (under short day condition)"
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Query Match 88.6%; Score 45.2; DB 10; Length 399;
Best Local Similarity 94.0%; Pred. No. 0.00073;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||
Db 346 GACGAGCTGCTGCGCGCTCGGTACAAAGGTGCGGTCTCGCATGCGC 395

RESULT 4

LOCUS AU222715 467 bp mRNA EST 30-JUL-2001
DEFINITION AU222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence.
ACCESSION AU222715
VERSION AU222715.1 GI:15008327
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 467)
Sasaki, T. and Yamamoto, K.
Rice cDNA from etiolated shoot (2001)
Unpublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'

Query Match 88.6%; Score 45.2; DB 10; Length 467;
Best Local Similarity 94.0%; Pred. No. 0.00073;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
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FEATURES

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Query Match 88.6%; Score 45.2; DB 10; Length 467;
Best Local Similarity 94.0%; Pred. No. 0.00073;
Matches 47; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 gacgagctgctgcgcgcgtcggtacaaaggtgcgcgcctccgacatgcc 50
|||||


```
|||||
Db 198 GACGAGTCTGCGCGCTCGGCTACAAGTGGCTGCGTCCGACATGGC 247
|||||

RESULT 5
BF268018 844 bp mRNA EST 09-MAR-2001
LOCUS HV_CEA0019J17f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
ACCESSION BF268018
VERSION BF268018.2 GI:13263734
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Nov 17, 2000 this sequence version replaced gi:11199013.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 587.
FEATURES
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/organism="Hordeum vulgare"
/cultivar="CI16155 (Mia13)"
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/clone="HV_CEA0019J17f"
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/tissue_type="seedling green leaf"
/lab_host="TJC121"
/notes="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
BASE COUNT 150 a 290 c 276 g 128 t
ORIGIN

Query Match 87.5%; Score 44.6; DB 11; Length 844;
Best Local Similarity 92.2%; Pred. No. 0.0011;
Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 gacagctgtgcgcgcgtcggtacaaagtgccgcctccacatggcg 51
|||||
Db 260 GACGAGTCTGCGCGCTCGGCTACAAGTGGCTGCGTCCGACATGGCG 310
|||||

RESULT 6
BF659955 711 bp mRNA EST 06-SEP-2000
LOCUS BE659955 Glycine max cDNA, mRNA sequence.
DEFINITION 1077 GmaxSC Glycine max cDNA, mRNA sequence.
ACCESSION BE659955
VERSION BE659955.1 GI:9985949
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS Harris,N., Chapman,B.P. and Gijzen,M.
TITLE Gene expression in developing soybean seed coats
JOURNAL Unpublished (2000)
COMMENT Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@agr.ca.
FEATURES
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/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
/tissue_type="Seed coats"
/lab_host="E. coli strain XL0LR"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developmental stage
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adapters were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for directional cloning into lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XL1 Blue MRF+. Inserts were then
subcloned by mass excision using ExAssist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XL0LR."
BASE COUNT 186 a 207 c 179 g 134 t 5 others
ORIGIN

Query Match 79.2%; Score 40.4; DB 10; Length 711;
Best Local Similarity 88.0%; Pred. No. 0.019;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 7
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LOCUS BE659954 Glycine max cDNA, mRNA sequence.
DEFINITION 746 GmaxSC Glycine max cDNA, mRNA sequence.
ACCESSION BE659954
VERSION BE659954.1 GI:9985948
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
AUTHORS Harris,N., Chapman,B.P. and Gijzen,M.
TITLE Gene expression in developing soybean seed coats
JOURNAL Unpublished (2000)
COMMENT Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@agr.ca.
FEATURES
source
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/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
/tissue_type="Seed coats"
/lab_host="E. coli strain XL0LR"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developmental stage
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adapters were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for directional cloning into lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XL1 Blue MRF+. Inserts were then
subcloned by mass excision using ExAssist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XL0LR."
BASE COUNT 186 a 207 c 179 g 134 t 5 others
ORIGIN
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Best Local Similarity 82.0%; Pred. No. 0.44;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 18:34:13 ; Search time 69.5 Seconds
(without alignments)
166.192 Million cell updates/sec

Title: US-09-485-529-105
Perfect score: 51
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	25.8	50.6	773	3	US-09-248-335-39
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14	23.4	45.9	1866	5	PCT-US91-00399-1
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16	22.8	44.7	8540	5	PCT-US96-05611A-12
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23	22.6	44.3	2088	5	PCT-US95-06639-1
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25	22.4	43.9	1164	1	US-08-087-772A-3
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ALIGNMENTS

RESULT 1
US-09-385-028-16
; Sequence 16, Application US/09385028
; Patent No. 6232106
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paraskar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6232106
; TITLE OF INVENTION: Acid Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
; STREET: The Jenifer Bulding, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/385,028
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 39305350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1542 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-385-028-16

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Db 207313 qtcgatgttctgtgtgcgcqctccgaagtcaagqgtgccaacaccactcgg 207361

FILING DATE: 08-NOV-1994

TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: RXR HUMAN ALPHA
FEATURE:
NAME/KEY: CDS
LOCATION: join(76..1464)
PCT-US91-00399-1

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RESULT 15
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Sequence 1, Application US/08440856A
Patent No. 5750873
GENERAL INFORMATION:
APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1517
TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-440-856A-1

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Search completed: December 19, 2001, 21:44:58
Job time: 11445 sec

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Date: Dec 19, 2001 11:20 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

Query: US-09-485-529-104

Query length: 17

Database: N_Geneseq_1101.*

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/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI60893	+	35.00	109.61	497.95	765	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAS08063	+	35.00	94.31	3.5e+03	3592
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/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT60094	+	35.00	109.40	536.24	811	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH54013	-	35.00	93.99	3.7e+03	3713
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/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC34294	+	35.00	108.82	551.39	829	1	/SIDS2/gcgdata/geneseq/NA1992.DAT:AAQ24856	-	35.00	93.35	4.0e+03	3959
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI59107	-	35.00	108.55	570.87	852	1	/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT86172	+	35.00	92.64	4.4e+03	4253
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC99941	+	35.00	108.39	582.80	866	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI58000	+	35.00	92.64	4.4e+03	4253
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC52465	+	35.00	108.14	601.65	886	1	/SIDS2/gcgdata/geneseq/NA1998.DAT:AAV52183	+	35.00	90.39	5.9e+03	5338
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT77777	+	35.00	108.01	611.99	900	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAF21074	-	35.00	90.20	6.0e+03	5441
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT60094	+	35.00	108.01	611.99	900	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAF21074	-	35.00	90.20	6.0e+03	5441
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC35289	+	35.00	107.34	666.85	963	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAF21074	-	35.00	90.20	6.0e+03	5441
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC34386	+	35.00	107.27	672.12	969	1	/SIDS2/gcgdata/geneseq/NA1998.DAT:AAV03311	-	35.00	90.06	6.1e+03	5510
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC50590	+	35.00	106.97	698.63	999	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF97891	-	35.00	89.71	6.4e+03	5720
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT77772	+	35.00	106.48	744.20	1050	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAF91919	+	35.00	88.64	7.3e+03	6373
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT77773	+	35.00	106.48	744.20	1050	1	/SIDS2/gcgdata/geneseq/NA1998.DAT:AAV14507	+	35.00	88.05	7.9e+03	6766
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT60089	+	35.00	106.48	744.20	1050	1	/SIDS2/gcgdata/geneseq/NA1992.DAT:AAV14517	+	35.00	88.05	7.9e+03	6768
/SIDS2/gcgdata/geneseq/NA1997.DAT:AAAT60090	+	35.00	106.48	744.20	1050	1	/SIDS2/gcgdata/geneseq/NA1998.DAT:AAV14517	+	35.00	88.05	7.9e+03	6768
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC54704	+	35.00	106.11	780.35	1090	1	/SIDS2/gcgdata/geneseq/NA1999.DAT:AAV99992	-	35.00	87.93	8.0e+03	6847
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC53558	+	35.00	106.09	782.17	1092	1	/SIDS2/gcgdata/geneseq/NA1999.DAT:AAZ21005	-	35.00	87.46	8.5e+03	7179
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH67414	+	35.00	105.62	831.57	1146	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC62115	+	35.00	87.28	8.7e+03	7316
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC33211	+	35.00	105.50	843.56	1159	1	/SIDS2/gcgdata/geneseq/NA1999.DAT:AAZ10081	+	35.00	85.84	1.0e+04	8455
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC47330	+	35.00	105.46	848.18	1164	1	/SIDS2/gcgdata/geneseq/NA1994.DAT:AAQJ66797	+	35.00	85.84	1.0e+04	8457
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC35165	+	35.00	105.42	852.80	1169	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAZ91920	+	35.00	85.69	1.1e+04	8590
/SIDS2/gcgdata/geneseq/NA1999.DAT:AAZ10675	+	35.00	105.25	871.36	1189	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAZ91916	+	35.00	85.42	1.1e+04	8827
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC54704	+	35.00	104.92	909.65	1230	1	/SIDS2/gcgdata/geneseq/NA1995.DAT:AAQJ98150	+	35.00	80.12	2.2e+04	1507
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC52338	+	35.00	104.84	919.05	1240	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH98476	+	35.00	79.70	2.3e+04	1573
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF17382	+	35.00	104.61	946.41	1269	1	/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAF21084	-	35.00	78.86	2.6e+04	1713
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/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC47931	-	35.00	104.01	1.0e+03	1348	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF28527	+	35.00	77.52	3.0e+04	1961
/SIDS2/gcgdata/geneseq/NA1999.DAT:AAAX05304	+	35.00	103.42	1.1e+03	1430	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH48110	-	35.00	68.31	9.7e+04	3499
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC46222	+	35.00	103.17	1.1e+03	1467	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH68529	-	35.00	49.01	8.7e+05	3499
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAZ60717	+	35.00	102.68	1.2e+03	1542	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH86531	+	35.00	49.01	8.7e+05	3499
/SIDS2/gcgdata/geneseq/NA1999.DAT:AAAF76734	+	35.00	102.35	1.3e+03	1594	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH68565	+	35.00	49.01	8.7e+05	3499
/SIDS2/gcgdata/geneseq/NA1995.DAT:AAQJ98669	+	35.00	101.33	1.4e+03	1767	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH68565	+	34.50	101.61	1.4e+03	1425
/SIDS2/gcgdata/geneseq/NA1998.DAT:AAV14449	+	35.00	101.13	1.5e+03	1804	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF1708	+	34.50	100.54	1.6e+03	1587
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF98421	+	35.00	101.13	1.5e+03	1804	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF1709	+	34.50	100.54	1.6e+03	1587
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/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC59457	+	35.00	101.10	1.5e+03	1809	1	/SIDS2/gcgdata/geneseq/NA1995.DAT:AAI13347	-	34.50	91.25	2.9e+03	4082
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC37661	+	35.00	101.09	1.5e+03	1811	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAAF28526	+	34.50	70.84	7.1e+04	3194
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI59099	-	35.00	100.86	1.5e+03	1854	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH48110	-	34.50	47.16	1.0e+06	3499
/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI60885	-	35.00	100.86	1.5e+03	1854	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAH48110	-	34.50	47.16	1.0e+06	3499
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC47422	-	35.00	100.49	1.6e+03	1923	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI20798	+	34.00	125.01	69.13	111
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAC38450	-	35.00	100.48	1.6e+03	1925	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI23971	+	34.00	125.01	69.13	111
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAFO7609	+	35.00	100.36	1.6e+03	1949	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI46028	+	34.00	125.01	69.13	111
/SIDS2/gcgdata/geneseq/NA2000.DAT:AAAT37325	+	35.00	100.33	1.6e+03	1956	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI49271	+	34.00	125.01	69.13	111
/SIDS2/gcgdata/geneseq/NA1989.DAT:AAAN91208	+	35.00	100.12	1.7e+03	1998	1	/SIDS2/gcgdata/geneseq/NA2001.DAT:AAI06506	+	34.00	125.01	69.13	111

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/SID2/cgcgdata/geneseq/NA2001.DAT:AAF31534	+	33.00	104.11	1.0e+03	631	1	/SID2/cgcgdata/geneseq/NA1997.DAT:AAF64505	+	33.00	97.76	2.3e+03	1200
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/SID2/cgcgdata/geneseq/NA2000.DAT:AAF10165	+	33.00	104.07	1.0e+03	634	1	/SID2/cgcgdata/geneseq/NA2001.DAT:AAF29042	+	33.00	97.68	2.3e+03	1209
/SID2/cgcgdata/geneseq/NA1997.DAT:AAAX23234	+	33.00	104.04	1.0e+03	636	1	/SID2/cgcgdata/geneseq/NA2000.DAT:AAZ97139	+	33.00	97.58	2.3e+03	1221
/SID2/cgcgdata/geneseq/NA1999.DAT:AAV13305	+	33.00	103.94	1.0e+03	642	1	/SID2/cgcgdata/geneseq/NA2001.DAT:AAAS22675	+	33.00	97.57	2.3e+03	1223
/SID2/cgcgdata/geneseq/NA2001.DAT:AAH88008	+	33.00	103.45	1.1e+03	646	1	/SID2/cgcgdata/geneseq/NA2000.DAT:AAAC90634	+	33.00	97.44	2.4e+03	1239
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/SID2/cgcgdata/geneseq/NA2000.DAT:AAAC37499	+	33.00	100.13	1.7e+03	944	1	/SID2/cgcgdata/geneseq/NA2000.DAT:AAAC45857	+	33.00	96.27	2.8e+03	1395
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/SID2/cgcgdata/geneseq/NA1999.DAT:AAAF63288	+	33.00	99.80	1.8e+03	976	1	/SID2/cgcgdata/geneseq/NA2001.DAT:AAH52003	+	33.00	95.91	2.9e+03	1446
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seq_documentation_block:
ID AAX36284 standard; DNA; 51 BP.

XX AAX36284;
XX 16-JUL-1999 (first entry)
XX Oligonucleotide derived from the wheat rht gene.
XX Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

OS Triticum aestivum.
XX WO9909174-A1.
XX 25-FEB-1999.
XX 07-AUG-1998; 98WO-GB02383.
XX 13-AUG-1997; 97GB-0017192.
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX Harberd NP, Peng J, Richards DE;
XX WPI; 1999-181040/15.
XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Claim 3; Page 53; 88pp; English.
XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is
CC derived from the wheat rht gene.

XX Sequence 51 BP; 7 A; 16 C; 21 G; 7 T; 0 other;

alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-485-529-104 x AAX36284 ..
Align seg 1/1 to: AAX36284 from: 1 to: 51
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
||||| 1 GAGGAGCTGCTGGCGCGCTCGGGTACAAGGTGCGCGCTCCGACATGCC 50
17 a 17
51 G 51

seq_name: /SID52/gcgcdata/geneseq/geneseqn/NA1999.DAT:AAH36263

seq_documentation_block:
ID AAX36263 standard; DNA; 453 BP.

XX AAX36263;
XX 16-JUL-1999 (first entry)
XX DNA sequence obtained after sequencing wheat Rht clone 14a1.
XX Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.
OS Triticum aestivum.
XX WO9909174-A1.
XX 25-FEB-1999.
XX 07-AUG-1998; 98WO-GB02383.
XX 13-AUG-1997; 97GB-0017192.
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX Harberd NP, Peng J, Richards DE;
XX WPI; 1999-181040/15.
XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 2b(9); 88pp; English.
XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence was
CC obtained after partially sequencing wheat Rht clone 14a1.

XX Sequence 453 BP; 85 A; 136 C; 158 G; 67 T; 7 other;

alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-485-529-104 x AAX36263 ..
Align seg 1/1 to: AAX36263 from: 1 to: 453
1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
273 GACGAGCTGCTGGCGGCTGGGTACAGGTGGCGGCTCCGACATGCG 322
17 a 17
|
323 G 323

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36279

seq_documentation_block:
ID AAX36279 standard; DNA; 2125 BP.
XX
AC AAX36279;
XX
DT 16-JUL-1999 (first entry)
XX
DE Wheat Rht clone 5a1 genomic sequence.
XX
KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.
XX
OS Triticum aestivum.
XX
PN WO9909174-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
DR WPI; 1999-181040/15.
XX
DR P-PSDB; AAY02540.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 8a; 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the wheat Rht clone 5a1 genomic sequence.
XX
SQ Sequence 2125 BP; 325 A; 768 C; 723 G; 309 T; 0 other;

alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-485-529-104 x AAX36279 ..
Align seg 1/1 to: AAX36279 from: 1 to: 2125
1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
139 GACGAGCTGCTGGCGGCTGGGTACAGGTGGCGGCTCCGACATGCG 188
17 a 17
|
189 G 189

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36275

seq_documentation_block:
ID AAX36275 standard; DNA; 2709 BP.
XX
AC AAX36275;
XX
DT 16-JUL-1999 (first entry)
XX
DE Composite DNA sequence of wheat Rht gene.
XX
KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.
XX
OS Triticum aestivum.
XX
PN WO9909174-A1.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
DR WPI; 1999-181040/15.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 3a; 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the composite DNA sequence of wheat Rht gene.
XX
SQ Sequence 2709 BP; 473 A; 900 C; 823 G; 482 T; 31 other;

alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

```

alignment_block:
US-09-485-529-104 x AAX36275  ..
Align seg 1/1 to: AAX36275 from: 1 to: 2709

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
273 GAGGAGCTGCTGGCGGCTCGGGTACAAGGTGCGGCTCCGACATGGC 322

17 a 17
|
323 G 323

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36281

seq_documentation_block:
ID AAX36281 standard; DNA; 302 BP.
XX
AC AAX36281;
XX
DT 16-JUL-1999 (first entry)
XX
DE Partial sequence of the maize D8-1 allele.
XX
KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; maize; ss.
XX
OS Zea mays.
XX
PN WO9909174-Al.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
DR WPI; 1999-181040/15.
DR P-PSDB; AAY02542.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 11a; 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the partial sequence of the maize D8-1 allele.
XX
SQ Sequence 302 BP; 52 A; 82 C; 123 G; 45 T; 0 other;

```

```

alignment_scores:
Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

```

```

alignment_block:
US-09-485-529-104 x AAX36281  ..
Align seg 1/1 to: AAX36281 from: 1 to: 302

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
100 GATGAGCTGCTGGCGGCTCGGGTACAAGGTGCGTTCGTCGGATATGGC 149

17 a 17
|
150 G 150

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36282

seq_documentation_block:
ID AAX36282 standard; DNA; 371 BP.
XX
AC AAX36282;
XX
DT 16-JUL-1999 (first entry)
XX
DE Partial sequence of the maize D8-2023 allele.
XX
KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; maize; ss.
XX
OS Zea mays.
XX
PN WO9909174-Al.
XX
PD 25-FEB-1999.
XX
PF 07-AUG-1998; 98WO-GB02383.
XX
PR 13-AUG-1997; 97GB-0017192.
XX
PA (PLAN-) PLANT BIOSCIENCE LTD.
XX
PI Harberd NP, Peng J, Richards DE;
XX
DR WPI; 1999-181040/15.
DR P-PSDB; AAY02543.
XX
PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
PS Disclosure; Fig 11c; 88pp; English.
XX
CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence represents
CC the partial sequence of the maize D8-2023 allele.
XX
SQ Sequence 371 BP; 56 A; 121 C; 139 G; 55 T; 0 other;

```

```

alignment_scores:
Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0

```


Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AAX36282 ..

Align seg 1/1 to: AAX36282 from: 1 to: 371

```
1 AspGluleuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
64 GAGGAGCTGCTGCGCGCTCGGGTACAGGTGCGTTCGGATATGGC 113
17 a 17
114 G 114
```

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36277

seq_documentation_block:

ID AAX36277 standard; DNA; 770 BP.

XX AC AAX36277;

DT 16-JUL-1999 (first entry)

DE Rice EST D39460 sequence, homologous to wheat Rht gene.

KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;

KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;

KW paclobutrazol; rice; expressed sequence tag; EST; ss.

OS Oryza sativa.

PN WO9909174-Al.

XX PD 25-FEB-1999.

XX PF 07-AUG-1998; 98WO-GB02383.

XX PR 13-AUG-1997; 97GB-0017192.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Harberd NP, Peng J, Richards DE;

DR WPI: 1999-181040/15.

DR P-PSDB; AAY02538.

PT New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is

PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Claim 13; Fig 6a; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents CC rice expressed sequence tag (EST) AAB39460, which is homologous to the wheat Rht gene.

XX Sequence 770 BP; 104 A; 252 C; 294 G; 120 T; 0 other;

alignment_scores:

Quality: 78.00 Length: 17

Ratio: 4.588 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AAX36277 ..

Align seg 1/1 to: AAX36277 from: 1 to: 770

```
1 AspGluleuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
114 GACGAGCTGCTGCGCGCTCGGGTACAAAGTGGCTGCGCATGGC 163
17 a 17
164 C 164
```

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT: AAX36280

seq_documentation_block:

ID AAX36280 standard; DNA; 2255 BP.

XX AC AAX36280;

DT 16-JUL-1999 (first entry)

DE Maize lal genomic clone sequence.

XX Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;

KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;

KW paclobutrazol; maize; ss.

OS Zea mays.

PN WO9909174-Al.

XX PD 25-FEB-1999.

XX PF 07-AUG-1998; 98WO-GB02383.

XX PR 13-AUG-1997; 97GB-0017192.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Harberd NP, Peng J, Richards DE;

DR WPI: 1999-181040/15.

DR P-PSDB; AAY02541.

PT New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is

PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 9a; 88pp; English.

XX The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents CC the maize lal genomic clone sequence.

XX Sequence 2255 BP; 334 A; 817 C; 737 G; 367 T; 0 other;

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
 US-09-485-529-104 x AAX36280 ..

Align seg 1/1 to: AAX36280 from: 1 to: 2255

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 308 GATGAGCTGCTGCGCGCTCGGGTACAAAGGTGCGTTCGGATATGCC 357
 17 a 17
 |
 358 G 358

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36276

seq_documentation_block:
 ID AAX36276 standard; DNA; 725 BP.

XX AC AAX36276;
 XX DT 16-JUL-1999 (first entry)
 XX DE Partial cDNA sequence of rice D39460 (a wheat Rht gene homologue).
 XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
 XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 XX KW paclobutrazol; ss.
 XX OS Oryza sativa.
 XX PN WO9909174-A1.
 XX PD 25-FEB-1999.
 XX PF 07-AUG-1998; 98WO-GB02383.
 XX PR 13-AUG-1997; 97GB-0017192.
 XX PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX PI Harberd NP, Peng J, Richards DE;
 XX WPI; 1999-181040/15.
 XX PS New Triticum Aestivum polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is
 PT antagonised by gibberellin, used to confer a dwarf phenotype
 XX Disclosure; Fig 4a; 89pp; English.
 XX CC The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in Triticum Aestivum, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence represents
 CC the partial cDNA sequence of rice AAD39460 (a wheat Rht gene homologue).
 XX SQ Sequence 725 BP; 98 A; 226 C; 276 G; 119 T; 6 other;

alignment_scores:
 Quality: 72.00 Length: 16
 Ratio: 4.500 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 93.750

alignment_block:
 US-09-485-529-104 x AAX36276 ..

Align seg 1/1 to: AAX36276 from: 1 to: 725

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 109 GAGCTGCTGCGCGCTCGGGTACAAAGGTGCGTTCGACATGCC 156

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36273

seq_documentation_block:
 ID AAX36273 standard; DNA; 324 BP.

XX AC AAX36273;
 XX DT 16-JUL-1999 (first entry)
 XX DE DNA sequence obtained after sequencing wheat Rht clone 5a1.
 XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
 XX KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 XX KW paclobutrazol; ss.
 XX OS Triticum aestivum.
 XX PN WO9909174-A1.
 XX PD 25-FEB-1999.
 XX PF 07-AUG-1998; 98WO-GB02383.
 XX PR 13-AUG-1997; 97GB-0017192.
 XX PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX PI Harberd NP, Peng J, Richards DE;
 XX WPI; 1999-181040/15.
 XX PS New Triticum Aestivum polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is
 PT antagonised by gibberellin, used to confer a dwarf phenotype
 XX Disclosure; Fig 2c(6); 88pp; English.
 XX CC The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in Triticum Aestivum, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence was
 CC obtained after partially sequencing wheat Rht clone 5a1.
 XX SQ Sequence 324 BP; 39 A; 141 C; 85 G; 56 T; 3 other;

alignment_scores:
 Quality: 70.00 Length: 15
 Ratio: 4.667 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

```
alignment_block:
US-09-485-529-104 x AAX36273/rev ..
Align seg 1/1 to reverse of: AAX36273 from: 1 to: 324

3 LeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
|||||
156 CTGCTGGCGGCGCTCGGTACAAGGTGCGCGCTCCGACATGGCG 112

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC65312
seq_documentation_block:
ID AAC65312 standard; cDNA; 457 BP.
XX AAC65312;
AC
XX
XX
DT 09-FEB-2001 (first entry)
XX
DE Arabidopsis SCL EST T22782.
XX
XX Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL;
KW transgenic plant; cell division; molecular marker; herbicide resistance;
KW salt resistance; pathogen resistance; insect resistance; ss.
XX
OS Arabidopsis thaliana.
XX
XX WO200053723-A2.
XX
XX 14-SEP-2000.
XX
XX 07-MAR-2000; 2000WO-US05875.
XX
XX 10-MAR-1999; 99US-0265585.
XX
XX (UUNY ) UNIV NEW YORK STATE.
XX
XX Benfey PN, Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysh L;
PI Helariutta Y, Bruce W, Lim J;
XX
XX WPI; 2000-594315/56.
XX
XX Scarecrow gene useful for producing transgenic plants expressing genes
PT whose product increases starch, lignin or cellulose biosynthesis and
PT confers herbicide, pathogen or insect resistance .
XX
XX Claim 6; Fig 28M; 200pp; English.
XX
XX The present sequence is given in a specification relating to the
CC structure and function of a regulatory gene, SCARECROW (SCR).
CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (VHID) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem
CC development and gravitropism of stem or hypocotyl is altered. Cell
CC division is increased or decreased in roots resulting in thicker or
CC thinner root development. The transgenic plants are useful for expressing
CC a gene of interest encoding a gene product that confers herbicide, salt,
CC pathogen or insect resistance in root or embryos and genes encoding
CC starch, lignin or cellulose biosynthesis in shoots. The SCR gene also
CC confers less susceptibility to lodging in the transgenic plants than a
CC wild-type plant. SCR gene sequences are also useful as molecular markers
CC for a quantitative trait e.g. root or gravitropism trait in molecular
CC breeding of crop plants.
XX
SQ Sequence 457 BP; 141 A; 86 C; 87 G; 125 T; 18 other;
```

```
alignment_scores:
Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353
```

```
alignment_block:
US-09-485-529-104 x AAC65312 ..
Align seg 1/1 to: AAC65312 from: 1 to: 457

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
|||||
256 GATGAGCTTCTAGCTGTCTTGGTTATAAGGTTAGGTCATCCGAAATGCG 305

17 a 17
306 T 306

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC45745
seq_documentation_block:
ID AAC45745 standard; DNA; 1602 BP.
XX AAC45745;
AC
XX
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47609.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
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XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 28-APR-1999; 99US-0131449.
XX 30-APR-1999; 99US-0132048.
XX 30-APR-1999; 99US-0132407.
XX 04-MAY-1999; 99US-0132484.
XX 05-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 06-MAY-1999; 99US-0132487.
XX 07-MAY-1999; 99US-0132863.
XX 11-MAY-1999; 99US-0134256.
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XX 14-MAY-1999; 99US-0134370.
XX 18-MAY-1999; 99US-0134768.
XX 19-MAY-1999; 99US-0134941.
XX 20-MAY-1999; 99US-0135124.
XX 21-MAY-1999; 99US-0135353.
XX 24-MAY-1999; 99US-0135629.
XX 25-MAY-1999; 99US-0136021.
XX 27-MAY-1999; 99US-0136392.
XX 28-MAY-1999; 99US-0136782.
XX 01-JUN-1999; 99US-0137222.
XX 03-JUN-1999; 99US-0137528.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 17-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139463.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140695.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
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PR 06-JUL-1999; 99US-0142390.
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PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
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PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
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PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
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PR 03-AUG-1999; 99US-0147038.
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PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
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PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
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PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353
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17 a 17
132 T 132

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT.AAD06661

seq_documentation_block:
ID AAD06661 standard; cDNA; 1764 BP.

XX AAD06661;
AC AAD06661;
XX 10-AUG-2001 (first entry)
XX A. thaliana transcription factor G308 homolog, G307 cDNA.

XX Plant transcription factor; phenotype: sugar sensing characteristic;
KW transgenic plant; plant yield; growth; germination; photosynthesis;
KW glyoxylate metabolism; respiration; pathogen response; wounding response;
KW cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW storage organ; metabolism; ss.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers
FH 1..1764
FT CDS /tag= a "Transcription factor homolog"
FT /product= "Transcription factor homolog"

XX WO200135725-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31414.

XX 17-NOV-1999; 99US-0166228.

XX 17-APR-2000; 2000US-0197899.

XX 22-AUG-2000; 2000US-0227439.

XX (MEND-) MENDEL BIOTECHNOLOGY INC.

PA (JIAN-) JIANG C.

PA (HEAR-) HEARD J.

PA (PINE-) PINEDA O.

PA (PILG-) PILGRIM M.

PA (ADAM-) ADAM L.

PA (RIEC-) RIECHMANN J L.

PA (YUGG-) YU G.

PA (SAMA-) SAMAHA R.

XX Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;

PI Yu G, Samaha R;

XX WPI; 2001-335977/35.

XX P-PSDB; AAE02560.

XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the sugar sensing characteristics of plants and increasing
PT yield, e.g. corn, potato and cotton plants -
XX
XX Claim 4; Page 113-115; 151pp; English.
XX
XX The patent relates to polynucleotides encoding 35 plant transcription

CC factors which may be used to modify phenotype associated with a plant's
CC sugar sensing characteristics and increasing yield when their expression
CC level is altered. Sugars are central regulatory molecules that control
CC aspects of physiology, metabolism and development. Therefore the cDNAs
CC and proteins of the invention are useful for modifying the growth and
CC germination rates of plants, photosynthesis, glyoxylate metabolism,
CC respiration, starch and sucrose synthesis and degradation, pathogen
CC response, wounding response, cell cycle regulation, pigmentation,
CC flowering and senescence of plants and for modifying sink-source
CC relationships in seeds, tubers, roots, and other storage organs leading
CC to an increase in yield. The transcription factor polynucleotides and
CC polypeptides may be used to alter the structure and developmental
CC characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC tobacco, tomato, watermelon, rosaceus fruits and/or vegetable brassicas.
CC The present sequence is a homolog of Arabidopsis thaliana transcription
CC factor cDNA.
XX
SQ Sequence 1764 BP; 431 A; 383 C; 448 G; 502 T; 0 other;

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Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 82.353

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180 G 180

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seq_documentation_block:

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XX AAD05776;

XX 31-JUL-2001 (first entry)

XX Arabidopsis thaliana transcription factor, G307 cDNA.

XX Transcription factor; biochemical characteristic; controlling element;
KW structural characteristic; developmental characteristic; gene therapy;
KW agricultural biotechnology; plant trait modification; ss.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 1..1764

FT /tag= a

FT /product= "Transcription factor, G307"

XX WO200136597-A1.

XX 25-MAY-2001.

XX 14-NOV-2000; 2000WO-US31344.

XX 17-NOV-1999; 99US-0166228.

XX 17-APR-2000; 2000US-0197899.

XX 22-AUG-2000; 2000US-0227439.

```
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (CREE/) CREELMAN R.
PA (YUGG/) YU G.
PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (HEAR/) HEARD J.
PA (SAMA/) SAMAHA R.
PA (PILG/) PILGRIM M.
PA (PINE/) PINEDA O.
PA (JIAN/) JIANG C.
XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
PI Pilgrim M, Pineda O, Jiang C;
XX WPI: 2001-335999/35.
DR P-PSDB: AAE01892.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the biochemical characteristics of plants e.g. corn,
PT potato and cotton plants -
XX
XX Claim 4; Page 66-68; 127pp: English.
XX
XX The present sequence is Arabidopsis thaliana transcription factor,
CC G307 cDNA. The transcription factor is used for altering a plant's
CC biochemical characteristics. The transcription factor may be used to
CC alter the structure and developmental characteristics of plants such as
CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,
CC alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry,
CC raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,
CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers,
CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,
CC rosaceous fruits and/or vegetable brassicas. Transcription factors are
CC key controlling elements of biological pathways and altering expression
CC levels of 1 or more transcription factors can change entire biological
CC pathways in an organism. Therefore manipulating transcription factor
CC levels in plants offers great potential in agricultural biotechnology
CC for modifying a plant's traits. Transcription factor cDNA is useful in
CC gene therapy.
XX
XX Sequence 1764 BP; 431 A; 383 C; 448 G; 502 T; 0 other;
SQ
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  Ratio: 4.118       Gaps: 0
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17 a 17
180 G 180
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seq_documentation_block:
ID AAD06646 standard; cDNA; 1951 BP.
XX
AC AAD06646;
XX
DT 10-AUG-2001 (first entry)
XX
DE A. thaliana transcription factor G308 cDNA.
XX
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KW Plant transcription factor; phenotype; sugar sensing characteristic;
KW transgenic plant; plant yield; growth; germination; photosynthesis;
KW glyoxylate metabolism; respiration; pathogen response; wounding response;
KW cell cycle regulation; pigmentation; flowering; senescence; physiology;
KW storage organ; metabolism; ss.
XX Arabidopsis thaliana.
OS
XX Key Location/Qualifiers
FH 196..1794
FT /*tag= a
FT /product= "Transcription factor"
XX WO200135725-A1.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US1414.
XX
XX 17-NOV-1999; 99US-0166228.
XX 17-APR-2000; 2000US-0197899.
XX 22-AUG-2000; 2000US-0227439.
XX
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J.
PA (PINE/) PINEDA O.
PA (PILG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (SAMA/) SAMAHA R.
XX
XX Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
PI Yu G, Samaha R;
XX
XX WPI: 2001-335977/35.
DR P-PSDB: AAE02545.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the sugar sensing characteristics of plants and increasing
PT yield, e.g. corn, potato and cotton plants -
XX
XX Claim 4; Page 72-74; 151pp: English.
XX
XX The patent relates to polynucleotides encoding 35 plant transcription
CC factors which may be used to modify phenotype associated with a plant's
CC sugar sensing characteristics and increasing yield when their expression
CC level is altered. Sugars are central regulatory molecules that control
CC aspects of physiology, metabolism and development. Therefore the cDNAs
CC and proteins of the invention are useful for modifying the growth and
CC germination rates of plants, photosynthesis, glyoxylate metabolism,
CC respiration, starch and sucrose synthesis and degradation, pathogen
CC response, wounding response, cell cycle regulation, pigmentation,
CC flowering and senescence of plants and for modifying sink-source
CC relationships in seeds, tubers, roots, and other storage organs leading
CC to an increase in yield. The transcription factor polynucleotides and
CC polypeptides may be used to alter the structure and developmental
CC characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
CC The present sequence is an Arabidopsis thaliana transcription factor
CC cDNA.
XX
XX Sequence 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;
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alignment_scores:
  Quality: 70.00      Length: 17
  Ratio: 4.118       Gaps: 0
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Percent Similarity: 100.000 Percent Identity: 82.353

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274 GATGAGCTTCTAGCTGTTCTTGGTTACAAAGTTAGGTCATCGGAATGGC 323

17 a 17
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324 T 324

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT: AAD05791

seq_documentation_block:
ID AAD05791 standard; cDNA; 1951 BP.
AC AAD05791;
DT 31-JUL-2001 (first entry)
XX Arabidopsis thaliana transcription factor, G308 cDNA.
DE
KW Transcription factor; biochemical characteristic; controlling element;
KW structural characteristic; developmental characteristic; gene therapy;
KW agricultural biotechnology; plant trait modification; ss.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 196..1794
FT /*tag= a
FT /product= "Transcription factor, G308"
XX
XX WO200136597-A1.
XX
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31344.
XX
XX 17-NOV-1999; 99US-0166228.
XX 17-APR-2000; 2000US-0197899.
XX 22-AUG-2000; 2000US-0227439.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
XX PA (CREE/) CREELMAN R.
XX PA (YUGG/) YU G.
XX PA (ADAM/) ADAM L.
XX PA (RIEC/) RIECHMANN J L.
XX PA (HEAR/) HEARD J.
XX PA (SAMA/) SAMAHA R.
XX PA (PILG/) PILGRIM M.
XX PA (PINE/) PINEDA O.
XX PA (JIAN/) JIANG C.
XX
XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
XX Pilgrim M, Pineda O, Jiang C;
XX
XX WPI: 2001-335999/35.
XX P-PSDB: AAE01907.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
XX PT for altering the biochemical characteristics of plants e.g. corn,
XX PT potato and cotton plants -
XX
XX Claim 4; Page 112-113; 127pp; English.
XX
XX The present sequence is Arabidopsis thaliana transcription factor, G308
XX cDNA, a homologue of G307. The transcription factor is used for altering
XX a plant's biochemical characteristics. The transcription factor may be

CC used to alter the structure and developmental characteristics of plants
CC such as soybean, wheat, corn, potato, cotton, rice, oilseed rape,
CC sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry,
CC strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber,
CC eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas,
CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,
CC watermelon, rosaceous fruits and/or vegetable brassicas. Transcription
CC factors are key controlling elements of biological pathways and altering
CC expression levels of 1 or more transcription factors can change entire
CC biological pathways in an organism. Therefore manipulating transcription
CC factor levels in plants offers great potential in agricultural
CC biotechnology for modifying a plant's traits. Transcription factor cDNA
XX is useful in gene therapy.
XX
SQ Sequence: 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;

alignment_scores:
Quality: 70.00 Length: 17
Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

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Align seg 1/1 to: AAD05791 from: 1 to: 1951

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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17 a 17
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324 T 324

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA1937.DAT: AAT91937

seq_documentation_block:
ID AAT91937 standard; DNA; 1964 BP.
XX
XX AAT91937;
XX
XX 19-MAR-1998 (first entry)
XX Arabidopsis thaliana gibberellin insensitivty gene gai.
DE
XX
XX Gibberellin insensitivity; gai; plant growth inhibition;
KW dwarf phenotype; lodging resistance; increased yield;
KW flowering regulation; bolting inhibition; spinach; lettuce;
KW antibody; identification; probe; primer; antisense; sense;
KW expression regulation; co-suppression; rice;
KW Bakane disease resistance; ss.
XX
XX Arabidopsis thaliana.
XX
XX WO9729123-A2.
XX
XX 14-AUG-1997.
XX
XX 12-FEB-1997; 97WO-GB00390.
XX
XX 12-FEB-1996; 96GB-0002796.
XX
XX (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
XX Carol P, Harberd NP, Peng J, Richards DE;
XX
XX WPI: 1997-415295/38.
XX P-PSDB: AAW30792.
XX
XX Nucleic acid encoding gibberellin inhibitor GAI and related
XX PT antisense sequences - used to create tall, or particularly, dwarf
XX PT plants, especially crops such as maize, rice and wheat

xx PS Claim 2; Fig 3; 76pp; English.

xx CC The present sequence encodes the Arabidopsis thaliana gibberellin
 CC insensitivity (gai) gene product (GAI), the expression of which
 CC inhibits plant growth. However the inhibition is antagonised by
 CC gibberellin (GA), while gai expression confers a dwarf phenotype
 CC that is insensitive to GA. Manipulating gai and GAI expression can
 CC produce tall or dwarf plants, particularly the latter for increased
 CC resistance to lodging and increased yield. It may also allow
 CC regulation of flowering, i.e. plants remain in the vegetative state
 CC until treated with GA, useful to inhibit bolting in spinach and
 CC lettuce. GAI can be used to raise specific antibodies for
 CC identifying homologous proteins or genes in other species. gai
 CC fragments can also be used as probes or primers to identify and
 CC clone related sequences, or in the preparation of antisense or
 CC sense expression regulating (co-suppressing) sequences. Rice plants
 CC that express GAI may be resistant to Bakane disease. Manipulation
 CC of gai and GAI makes it possible to tailor the degree of dwarfism
 CC and GA sensitivity to particular crops or situations.
 xx SQ Sequence 1964 BP; 489 A; 426 C; 474 G; 575 T; 0 other;

alignment_scores:
 Quality: 70.00 Length: 17
 Ratio: 4.118 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x AAT91937 ..

Align seg 1/1 to: AAT91937 from: 1 to: 1964

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17 a 17
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 337 T 337

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:AAF25480

seq_documentation_block:

ID AAF25480 standard; DNA; 1779 BP.

xx AC AAF25480;

xx DT 15-MAY-2001 (first entry)

xx DE Nucleotide sequence of a wildtype GRAS protein.

xx KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
 xx plant development; dwarf plant; crucifer; ss.

xx OS Brassica napus.

xx FH Key Location/Qualifiers
 xx CDS 60..1778
 xx FT /*tag= a
 xx FT /product= "GRAS"

xx PN WO200109356-A1.

xx XX 08-FEB-2001.

xx XX 02-AUG-2000; 2000WO-FR02216.

xx XX 02-AUG-1999; 99FR-0010023.

xx PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

xx XX

PI Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
 xx XX WPI: 2001-182964/18.
 DR P-PSDB; AAB31883.
 xx XX New mutant nucleic acid encoding modified GRAS family protein, used to
 PT produce dwarf transgenic plants -
 PT xx
 xx PS Example 1; Page 13-15; 28pp; French.

xx CC The present sequence encodes a wild type plant protein of the GRAS
 CC family. The specification describes a mutant allele of the BZH gene, the
 CC which contains a G1695A mutation resulting in the mutation E546K in the
 CC protein. GRAS proteins are transcription factors implicated in
 CC regulation of the response to gibberellins and thus in control of
 CC morphogenesis and plant development. The mutant GRAS protein is
 CC used to produce dwarf plants, specifically crucifers. Dwarf plants may
 CC be sown earlier (increasing nitrate accumulation without risking
 CC excessive stem growth during winter), and have better resistance to
 CC cold and lodging. They are also easier to harvest and allow for better
 CC monitoring of the crop.

xx SQ Sequence 1779 BP; 418 A; 430 C; 476 G; 455 T; 0 other;

alignment_scores:
 Quality: 66.00 Length: 17
 Ratio: 3.882 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x AAF25480 ..

Align seg 1/1 to: AAF25480 from: 1 to: 1779

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 |||||
 183 GACGAGCTTCTAGGAGTCTTGGTTACAAAGGTTAGGCTTCGGAGATGCG 232

17 a 17
 |
 233 T 233

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:AAF25481

seq_documentation_block:

ID AAF25481 standard; DNA; 1779 BP.

xx AC AAF25481;

xx DT 15-MAY-2001 (first entry)

xx DE Nucleotide sequence of a mutant GRAS protein.

xx KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
 xx plant development; dwarf plant; crucifer; ss.

xx OS Brassica napus.

xx FH Key Location/Qualifiers
 xx CDS 60..1778
 xx FT /*tag= a
 xx FT /product= "GRAS"

xx PN WO200109356-A1.

xx XX 08-FEB-2001.

xx XX 02-AUG-2000; 2000WO-FR02216.

xx XX 02-AUG-1999; 99FR-0010023.

xx PA (INRG) INRA INST NAT RECH AGRONOMIQUE.

xx XX

XX Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
 XX WPI; 2001-182964/18.
 DR P-PSDB; AAB31864.
 XX
 XX New mutant nucleic acid encoding modified GRAS family protein, used to
 PT produce dwarf transgenic plants -
 PT Example 1; Page 18-20; 28pp; French.
 PS
 XX The present sequence encodes a mutant plant protein of the GRAS
 CC family. The mutant allele of the B2H gene contains a G1695A mutation
 CC resulting in the mutation E546K in the protein. GRAS proteins are
 CC transcription factors implicated in regulation of the response to
 CC gibberellins and thus in control of morphogenesis and plant development.
 CC The mutant GRAS protein is used to produce dwarf plants, specifically
 CC crucifers. Dwarf plants may be sown earlier (increasing nitrate
 CC accumulation without risking excessive stem growth during winter), and
 CC have better resistance to cold and lodging. They are also easier to
 CC harvest and allow for better monitoring of the crop.
 XX
 SQ Sequence 1779 BP; 419 A; 430 C; 475 G; 455 T; 0 other;

alignment_scores:
 Quality: 66.00 Length: 17
 Ratio: 3.882 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 76.471
 alignment_block:
 US-09-485-529-104 x AAF25481 ..
 Align seg 1/1 to: AAF25481 from: 1 to: 1779
 1 AspGluLeuLeuAlaLaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 |||||
 183 GACGAGCTCTAGGAGTCTTGGGTACAAAGTTAGGTCTTCGGAGATGCG 232

17 a 17
 |
 233 T 233

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AA36266

seq_documentation_block:
 ID AAX36266 standard; DNA; 200 BP.
 XX
 AC AAX36266;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE DNA sequence obtained after sequencing wheat Rht clone 14a1.
 XX
 KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
 KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 KW paclobutrazol; ss.
 XX
 OS Triticum aestivum.
 XX
 PN WO9909174-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 07-AUG-1998; 98WO-GB02383.
 XX
 PR 13-AUG-1997; 97GB-0017192.
 XX
 PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX
 PI Harberd NP, Peng J, Richards DE;
 XX
 XX WPI; 1999-181040/15.
 DR

XX New Triticum Aestivum polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is
 PT antagonised by gibberellin, used to confer a dwarf phenotype
 XX
 PS Disclosure; Fig 2b(12); 88pp; English.
 XX
 CC The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in Triticum Aestivum, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence was
 CC obtained after partially sequencing wheat Rht clone 14a1.
 XX
 SQ Sequence 200 BP; 24 A; 58 C; 84 G; 27 T; 7 other;

alignment_scores:
 Quality: 65.00 Length: 15
 Ratio: 4.643 Gaps: 0
 Percent Similarity: 93.333 Percent Identity: 93.333
 alignment_block:
 US-09-485-529-104 x AAX36266 ..
 Align seg 1/1 to: AAX36266 from: 1 to: 200
 1 AspGluLeuLeuAlaLaLeuGlyTyrLysValArgAlaSerAsp 15
 |||||
 79 GACTATCTGCTGCGCGCTCGGTACAAAGTGCAGCGCTCCGAC 123

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AA36283

seq_documentation_block:
 ID AAX36283 standard; DNA; 416 BP.
 XX
 AC AAX36283;
 XX
 DT 16-JUL-1999 (first entry)
 XX
 DE Partial sequence of the wheat rht-10 allele.
 XX
 KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
 KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 KW paclobutrazol; ss.
 XX
 OS Triticum aestivum.
 XX
 PN WO9909174-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 07-AUG-1998; 98WO-GB02383.
 XX
 PR 13-AUG-1997; 97GB-0017192.
 XX
 PA (PLAN-) PLANT BIOSCIENCE LTD.
 XX
 PI Harberd NP, Peng J, Richards DE;
 XX
 DR WPI; 1999-181040/15.
 DR P-PSDB; AAY02544.
 XX
 PT New Triticum Aestivum polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is

PT antagonised by gibberellin, used to confer a dwarf phenotype
 PS Disclosure; Fig 12a; 88pp; English.

CC The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence represents
 CC the partial sequence of the wheat rht-10 allele.

SQ Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other;

alignment_scores:
 Quality: 62.00 Length: 13
 Ratio: 4.769 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-485-529-104 x AAX36283 ..

Align seg 1/1 to: AAX36283 from: 1 to: 416

5 AlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
 1 GCGGCGCTCGGGTACAAAGGTGCGCGCTCGACATGGCG 39

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36261

seq_documentation_block:

ID AAX36261 standard; DNA; 309 BP.

AC AAX36261;

DT 16-JUL-1999 (first entry)

DE DNA sequence obtained after sequencing wheat Rht clone 14a1.

KW Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;
 KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 KW paclobutrazol; ss.

OS *Triticum aestivum*.

PN WO9909174-A1.

PD 25-FEB-1999.

PF 07-AUG-1998; 98WO-GB02383.

PR 13-AUG-1997; 97GB-0017192.

PA (PLAN-) PLANT BIOSCIENCE LTD.

PI Harberd NP, Peng J, Richards DE;

DR WPI; 1999-181040/15.

PT New *Triticum aestivum* polynucleotides - encode a polypeptide which
 PT provides inhibition of the growth of plants, which inhibition is
 PT antagonised by gibberellin, used to confer a dwarf phenotype

PS Disclosure; Fig 2b(7); 88pp; English.

CC The specification describes polypeptides encoded by the Rht gene (and
 CC its homologues) that, when expressed in *Triticum aestivum*, inhibit
 CC growth of the plant. This growth inhibition is antagonised by
 CC gibberellin. The products can be used to provide Rht expression in
 CC plants, conferring a dwarf phenotype on a plant which is correctable
 CC by treatment with gibberellin. In addition, the products can be
 CC used to produce Rht mutant plants which are dwarfed compared with
 CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
 CC may be made by knocking out Rht or the relevant homologous gene in
 CC the plant of interest. Plants may be made which are resistant to
 CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
 CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
 CC dwarf but let crop plants grow tall. The present sequence was
 CC obtained after partially sequencing wheat Rht clone 14a1.

SQ Sequence 309 BP; 47 A; 102 C; 102 G; 45 T; 13 other;

alignment_scores:
 Quality: 46.00 Length: 9
 Ratio: 5.111 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-485-529-104 x AAX36261 ..

Align seg 1/1 to: AAX36261 from: 1 to: 309

8 GlyTyrLysValArgAlaSerAspMet 16
 18 GGGTACAAGGTGCGCGCTCCGACATG 44

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT86824

seq_documentation_block:

ID AAT86824 standard; cDNA; 817 BP.

AC AAT86824;

DT 09-JAN-1998 (first entry)

DE Hevea brasiliensis (S)-hydroxynitrilase cDNA.

KW (S)-hydroxynitrilase; production; (S)-cyanohydrin; aldehyde;
 KW hydrogen cyanide; recombinant; ss.

OS Hevea brasiliensis.

FH Key Location/Qualifiers
 FT CDS 44..817
 FT /*tag= a
 FT /product= (S)-hydroxynitrilase

PN DE19529116-A1.

PD 06-MAR-1997.

PF 08-AUG-1995; 95DE-1029116.

PR 08-AUG-1995; 95DE-1029116.

PA (OSTS) CHEMIE LINZ DEUT GMBH IL.

DR WPI; 1997-155423/15.

DR P-PSDB; AAW29164.

PT DNA encoding Hevea brasiliensis (S)-hydroxynitrilase - useful for
 PT production of cyanohydrin(s) from aldehyde and hydrogen cyanide

PS Claim 2; Page 8; 8pp; German.

CC The present sequence encodes Hevea brasiliensis
 CC (S)-hydroxynitrilase (S-HN), useful in the production of

CC (S)-cyanohydrins from aldehyde and hydrogen cyanide. Recombinantly
 CC produced S-HN has higher specific activity than native S-HN,
 CC probably due to post translational modification differences
 CC between plants and microorganisms.
 CC S-HN was isolated from H. brasiliensis leaves by homogenisation,
 CC followed by sequential chromatography on QAE-Sepharose FF,
 CC Phenyl-Sepharose and BioGel P180. A cDNA bank from the same source
 CC was prepared and screened with polyclonal rabbit antiserum raised
 CC against the isolated enzyme. The insert, about 1.1 kb, in the
 CC single positive clone was cloned into pHL100 and sequenced.
 XX
 SQ Sequence 817 BP; 250 A; 159 C; 193 G; 215 T; 0 other;

alignment_scores:
 Quality: 45.00 Length: 15
 Ratio: 3.750 Gaps: 0
 Percent Similarity: 80.000 Percent Identity: 66.667

alignment_block:

US-09-485-529-104 x AAT86824 ..

Align seg 1/1 to: AAT86824 from: 1 to: 817

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
 ||||| |||||:::||||| || |||||:::|||||
 116 CTCCTGTGAGGCACCTGGCCACAGCTTACTGCACCTGGACCTTGCA 160

seq_name: /SDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT36351

seq_documentation_block:

ID AAT36351 standard; cDNA; 1091 BP.

XX AAT36351;

DT 29-OCT-1997 (first entry)

DE Hevea brasiliensis S-hydroxynitrilase cDNA.

KW S-hydroxynitrilase; chiral synthesis; aliphatic; aromatic;

KW S-cyanohydrin; recombinant; ss.

XX Hevea brasiliensis.

FH Key Location/Qualifiers

FT CDS 57..830

FT /*tag= a

FT /product= S-hydroxynitrilase

XX WO9703204-A2.

XX 30-JAN-1997.

XX 10-JUL-1996; 96WO-EP03010.

XX 12-JUL-1995; 95AT-0001182.

XX (STAM) DSM CHEMIE LINZ GMBH.

XX Griengl H, Hasslacher M, Hayn EM, Kohlwein S, Schall M;
 PI Schwab H;

XX WPI; 1997-119058/11.

XX P-PSDB; AAW10593.

XX Hevea brasiliensis S-hydroxynitrilase - and recombinant equivalent
 PT of high specific activity, for chiral synthesis of cyano:hydrin(s)

XX Claim 2; Pages 2-3; 14pp; German.

XX The present sequence encodes the Hevea brasiliensis

CC S-hydroxynitrilase (S-HN), which can be used for the chiral

CC synthesis of aliphatic or aromatic S-cyanohydrins from HCN, or its

CC donor, and ketone. Recombinant S-HN has higher specific activity
 CC than the native enzyme.
 CC H. brasiliensis leaves were homogenised in cold pH 6.5 K phosphate
 CC buffer, and the extract subjected to sequential chromatography on
 CC QAE-Sepharose, Phenyl-Sepharose and BioGel 150 to recover a protein
 CC with a specific activity of 19 IU/mg.
 CC A cDNA library was prepared with polyclonal rabbit antiserum raised
 CC against the purified enzyme. The insert in one positive clone was
 CC isolated, and ligated into pBluescript to form pHL100. This
 CC plasmid, in E. coli SOLR, expressed a fusion protein with lacZ that
 CC was immunoreactive. Sequencing showed that the insert in this
 CC plasmid was not complete, and the missing 5'-end generated by 2
 CC stage PCR, resulting in plasmid pHL101, containing the entire
 CC coding sequence.
 XX
 SQ Sequence 1091 BP; 326 A; 196 C; 239 G; 330 T; 0 other;

alignment_scores:
 Quality: 45.00 Length: 15
 Ratio: 3.750 Gaps: 0
 Percent Similarity: 80.000 Percent Identity: 66.667

alignment_block:

US-09-485-529-104 x AAT36351 ..

Align seg 1/1 to: AAT36351 from: 1 to: 1091

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
 ||||| |||||:::||||| || |||||:::|||||
 129 CTCCTGTGAGGCACCTGGCCACAGCTTACTGCACCTGGACCTTGCA 173

seq_name: /SDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV36418

seq_documentation_block:

ID AAV36418 standard; cDNA; 1458 BP.

XX AAV36418;

DT 14-SEP-1998 (first entry)

DE Keratan sulphate 6-sulphotransferase.

KW K5GAL6ST; keratan sulphate 6-sulphotransferase; hybridization;

KW chick chondroitin 6-sulphotransferase; C6ST; phage Lambda;

KW expression vector; COS-7 cells; Bluescript plasmid; galactose;

XX keratan sulphate; chondroitin; ss.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1236

FT /*tag= a

FT /product= "Keratan sulphate 6-sulphotransferase"

XX EP845533-A2.

XX 03-JUN-1998.

XX 27-NOV-1997; 97EP-0309564.

XX 29-NOV-1996; 96JP-0320535.

XX (SEKG) SEIKAGAKU KOGYO CO LTD.

XX Fukuta M, Habuchi O;

XX WPI; 1998-288750/26.

XX P-PSDB; AAW61100.

XX Keratan sulphate 6-sulpho-transferase polypeptide - transfers
 PT sulphate from sulphate donor to galactose 6-hydroxy group etc.

alignment_scores:
Quality: 43.00 Length: 9
Ratio: 4.778 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.889

alignment_block:
US-09-485-529-104 x AAX36248 ..

Align seg 1/1 to: AAX36248 from: 1 to: 29

8 GlyTyrLysValArgAlaSerAspMet 16
|||||
3 GGGTACAGGTGCGTTCGCGATG 29

seq_name: /SIDS2/gcdata/geneseq/geneeqn/NA2000.DAT: AAC47519

seq_documentation_block:

ID AAC47519 standard; DNA; 864 BP.

XX

AC AAC47519;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54118.

XX

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 07-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.

PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 14-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 21-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

||||| ::| ||||| ||::| |||||
84 GAATATTGAACGTCAAAGTTATCTCTGTTAAAGCATCCGAT 125

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ10092

seq_documentation_block:
ID AAZ10092 standard; DNA; 235 BP.

XX AAZ10092;
XX
XX 28-OCT-1999 (first entry)
XX
XX Choristoneura biennis entomopoxvirus spheroidin-like gene sequence.
DE
XX
XX Spheroidin; Entomopoxvirus; expression system; replication;
KW heterologous gene expression; thymidine kinase; poxvirus; vaccinia;
KW swinepox virus; insect pest control; immunity; ss.
XX
XX Choristoneura biennis entomopoxvirus.
OS
XX
XX US5935777-A.
PN
XX
XX 10-AUG-1999.
PD
XX
XX 17-OCT-1995; 95US-0544332.
PF
XX
XX 17-OCT-1995; 95US-0544332.
PR
XX 19-FEB-1991; 91US-0657584.
PR
XX 30-JAN-1992; 92US-0827885.
PR
XX 12-FEB-1992; 92WO-US00855.
PR
XX 07-DEC-1992; 92US-0991867.
XX
XX (UYFL) UNIV FLORIDA RES FOUND INC.
PA
XX
XX Gruid ME, Hall RL, Li Y, Moyer RW;
PI
XX
XX WPI; 1999-457596/38.
DR
XX
XX P-PSDB; AAY30179.
DR
XX
XX Novel expression system for the expression of heterologous sequences
PT
XX
XX In insect and mammalian host cells
PT
XX
XX Example 10; Column 99-102; 72pp; English.

CC The present sequence represents an Entomopoxvirus (EPV) spheroidin-like
CC gene sequence. It is used to make the expression systems of the
CC invention. The specification describes an EPV expression system that
CC is capable of directing the replication and expression of a heterologous
CC gene in a selected host cell. The expression system comprises an EPV
CC promoter sequence operably linked to the selected heterologous gene
CC sequence. The expression system is used for the expression of
CC heterologous sequences and the production of selected proteins in
CC insect and mammalian host cells e.g. human, rodent and primate cells.
CC EPV thymidine kinase and spheroidin genes can also be used in
CC vertebrate poxviruses such as vaccinia and swinepox virus. The
CC expression vectors can also be used for the control of insect pests
CC through the insertion of a gene encoding an insect toxin into the
CC expression vector which will infect the target pest and produce large
CC quantities of the toxin. Spheroidin and thymidine kinase are nonessential
CC proteins which makes them ideal for the insertion of exogenous DNA and
CC they are capable of operating in a vertebrate poxvirus (e.g. vaccinia)-
CC mammalian cell expression vector system. Pox viruses are able to
CC stimulate cell-mediated and humoral immunity.
XX
XX Sequence 235 BP; 96 A; 20 C; 42 G; 77 T; 0 other;

alignment_scores:
Quality: 41.00 Length: 14
Ratio: 3.727 Gaps: 0
Percent Similarity: 78.571 Percent Identity: 64.286

alignment_block:

US-09-485-529-104 x AAZ10092 ..

Align seg 1/1 to: AAZ10092 from: 1 to: 235

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
||||| ::| ||||| ||::| |||||
84 GAATATTGAACGTCAAAGTTATCTCTGTTAAAGCATCCGAT 125

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:AAZ10093

seq_documentation_block:
ID AAZ10093 standard; DNA; 235 BP.

XX AAZ10093;
XX
XX 28-OCT-1999 (first entry)
XX
XX Choristoneura fumiferana entomopoxvirus spheroidin-like gene sequence.
DE
XX
XX Spheroidin; Entomopoxvirus; expression system; replication;
KW heterologous gene expression; thymidine kinase; poxvirus; vaccinia;
KW swinepox virus; insect pest control; immunity; ss.
XX
XX Choristoneura fumiferana entomopoxvirus.
OS
XX
XX US5935777-A.
PN
XX
XX 10-AUG-1999.
PD
XX
XX 17-OCT-1995; 95US-0544332.
PF
XX
XX 17-OCT-1995; 95US-0544332.
PR
XX 19-FEB-1991; 91US-0657584.
PR
XX 30-JAN-1992; 92US-0827885.
PR
XX 12-FEB-1992; 92WO-US00855.
PR
XX 07-DEC-1992; 92US-0991867.
XX
XX (UYFL) UNIV FLORIDA RES FOUND INC.
PA
XX
XX Gruid ME, Hall RL, Li Y, Moyer RW;
PI
XX
XX WPI; 1999-457596/38.
DR
XX
XX P-PSDB; AAY30180.
DR
XX
XX Novel expression system for the expression of heterologous sequences
PT
XX
XX In insect and mammalian host cells
PT
XX
XX Example 10; Column 101-102; 72pp; English.

CC The present sequence represents an Entomopoxvirus (EPV) spheroidin-like
CC gene sequence. It is used to make the expression systems of the
CC invention. The specification describes an EPV expression system that
CC is capable of directing the replication and expression of a heterologous
CC gene in a selected host cell. The expression system comprises an EPV
CC promoter sequence operably linked to the selected heterologous gene
CC sequence. The expression system is used for the expression of
CC heterologous sequences and the production of selected proteins in
CC insect and mammalian host cells e.g. human, rodent and primate cells.
CC EPV thymidine kinase and spheroidin genes can also be used in
CC vertebrate poxviruses such as vaccinia and swinepox virus. The
CC expression vectors can also be used for the control of insect pests
CC through the insertion of a gene encoding an insect toxin into the
CC expression vector which will infect the target pest and produce large
CC quantities of the toxin. Spheroidin and thymidine kinase are nonessential
CC proteins which makes them ideal for the insertion of exogenous DNA and
CC they are capable of operating in a vertebrate poxvirus (e.g. vaccinia)-
CC mammalian cell expression vector system. Pox viruses are able to
CC stimulate cell-mediated and humoral immunity.
XX
XX Sequence 235 BP; 95 A; 25 C; 42 G; 73 T; 0 other;

alignment_scores:

Quality: 41.00 Length: 14
Ratio: 3.727 Gaps: 0
Percent Similarity: 78.571 Percent Identity: 64.286

alignment_block:

US-09-485-529-104 x AAZ10093

Align seg 1/1 to: AAZ10093 from: 1 to: 235

2 GluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
||||||| :||| ||||| ||||| ||||| |||||
84 GAATTATGAACTCAAGGTTATCTCTGTTAAAGCATCCGAT 125

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:AA36271

seq_documentation_block:

ID AAX36271 standard; DNA; 285 BP.

XX AC AAX36271;

XX DT 16-JUL-1999 (first entry)

DE DNA sequence obtained after sequencing wheat Rht clone 5a1.

KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol; ss.

OS Triticum aestivum.

XX WO9909174-A1.

XX PD 25-FEB-1999.

XX PF 07-AUG-1998; 98WO-GB02383.

XX PR 13-AUG-1997; 97GB-0017192.

XX PA (PLAN-) PLANT BIOSCIENCE LTD.

XX PI Harberd NP, Peng J, Richards DE;

XX DR WPI; 1999-181040/15.

XX PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype

XX PS Disclosure: Fig 2c(4); 88pp; English.

CC The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence was
CC obtained after partially sequencing wheat Rht clone 5a1.

XX SQ Sequence 285 BP; 39 A; 89 C; 100 G; 46 T; 11 other;

alignment_scores:

Quality: 41.00 Length: 9
Ratio: 5.125 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 88.889

alignment_block:

US-09-485-529-104 x AAX36271/rev

Align seg 1/1 to reverse of: AAX36271 from: 1 to: 285

8 GlyTyrLysValArgAlaSerAspMet 16
||||||| ||||| ||||| ||||| |||||
283 GGGTACAGGCGCGCATCGACATG 257

seq_name: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:AAH99418

seq_documentation_block:

ID AAH99418 standard; cDNA; 556 BP.

XX AC AAH99418;

XX DT 16-OCT-2001 (first entry)

XX DE Human protein encoding cDNA sequence SEQ ID NO:253.

XX KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiagregant; haemostatic; vulnery; antituler; osteopathic; eczema;
KW dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.

XX OS Homo sapiens.

XX WO200153455-A2.

XX PD 26-JUL-2001.

XX PF 22-DEC-2000; 2000WO-US35017.

XX PR 23-DEC-1999; 99US-0471275.

XX PR 21-JAN-2000; 2000US-0488725.

XX PR 25-APR-2000; 2000US-0552317.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457603/49.

XX P-PSDB; AAM25477.

XX PT Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -

XX PS Claim 1; Page 410; 1217pp; English.

XX CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnery;
CC antituler; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production, the proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,

CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, ulcers,
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 CC Alzheimer's disease, parkinson's disease, neurodegenerative and
 CC neurological disorders.

XX
 SQ Sequence 556 BP; 153 A; 125 C; 128 G; 150 T; 0 other;

alignment_scores:

Quality: 41.00 Length: 14
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 92.857 Percent Identity: 50.000

alignment_block:

US-09-485-529-104 x AAH99418/rev ..

Align seg 1/1 to reverse of: AAH99418 from: 1 to: 556

3 LeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMet 16

.....
 294 ATGATGGCAGCATTTGGGATACAGTGTGAAAAGCAGCACATTG 253

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH81463

seq_documentation_block:

ID AAH81463 standard; DNA; 1476 BP.

XX AAH81463;

XX 21-SEP-2001 (first entry)

XX Escherichia coli protein encoding nucleotide sequence SEQ ID NO:262.

XX Escherichia coli; identification; proliferation; microorganism;

KW antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis;

KW bacterial growth inhibition; ds.

XX Escherichia coli.

XX WO200148209-A2.

XX 05-JUL-2001.

XX 19-DEC-2000; 2000WO-US34419.

XX 23-DEC-1999; 99US-0173005.

XX (ELIT-) ELITRA PHARM INC.

XX Forsyth RA, Ohlsen KL, Zyskind JW;

XX WPI: 2001-457376/49.

XX P-PSDB; AAG98407.

XX Novel nucleic acids encoding proteins required for Escherichia coli

XX proliferation, useful for screening for antimicrobial agents -

XX Claim 9; Page 393-395; 596pp; English.

XX The present invention describes a purified or isolated nucleic acid
 CC sequence (I) consisting essentially of one of the 93 nucleotide sequences
 CC given in AAH81202 to AAH81294, where expression of the nucleic acid in a
 CC microorganism is capable of inhibiting proliferation of a microorganism.
 CC (I) have antibacterial and antibiotic activities, and can be used in
 CC gene therapy. Expression of (I) in a microorganism inhibits proliferation
 CC of the microorganism, and the manufactured antibiotic is useful for
 CC reducing the activity or level of a gene product required for
 CC proliferation of a microorganism in a subject, specifically humans. The
 CC nucleic acids that inhibit bacterial growth or proliferation can be used

CC as antisense therapeutics for killing bacteria. In addition to
 CC therapeutic applications, the nucleic acid sequences complementary to
 CC sequences required for proliferation can be used as diagnostic tools.
 CC For example, nucleic acid probes complementary to proliferation-required
 CC sequences that are specific for particular species of microorganisms can
 CC be used as probes to identify particular microorganism species in
 CC clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli
 CC proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491
 CC represent oligonucleotides, which are used in the exemplification of the
 CC present invention.

XX
 SQ Sequence 1476 BP; 330 A; 372 C; 436 G; 338 T; 0 other;

alignment_scores:

Quality: 41.00 Length: 16
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 81.250 Percent Identity: 50.000

alignment_block:

US-09-485-529-104 x AAH81463 ..

Align seg 1/1 to: AAH81463 from: 1 to: 1476

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17

.....
 109 GAAGTTCGGCCAAATGAAGGTTATCAGATCAGTGGTCCGATTTAGCG 156

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ53179

seq_documentation_block:

ID AAZ53179 standard; DNA; 1521 BP.

XX AAZ53179;

XX 21-MAR-2000 (first entry)

XX Neisseria gonorrhoeae ORF 092 partial DNA sequence SEQ ID NO:309.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;

KW antibacterial; gene therapy; ds.

XX Neisseria gonorrhoeae.

XX WO9957280-A2.

XX 11-NOV-1999.

XX 30-APR-1999; 99WO-US09346.

XX 01-MAY-1998; 98US-0083758.

XX 31-JUL-1998; 98US-0094869.

XX 02-SEP-1998; 98US-0098994.

XX 02-SEP-1998; 98US-0099062.

XX 09-OCT-1998; 98US-0103749.

XX 09-OCT-1998; 98US-0103794.

XX 25-FEB-1999; 98US-0103796.

XX (CHIR) CHIRON CORP.

XX (GENO-) INST GENOMIC RES.

XX

XX Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;

PI Petersen J, Piazza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;

PI Tettelin H, Venter JC;

XX WPI: 2000-062150/05.

XX P-PSDB; AAY74417.

XX Novel Neisserial polypeptides predicted to be useful antigens for

XX vaccines and diagnostics -

XX

```

PS Claim 7; Page 288; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AA254615 to AA254615, and AA254615 to AA254615
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254616 to AA254616 to AA254616
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisseria meningitidis (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria meningitidis, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 1521 BP; 359 A; 430 C; 394 G; 338 T; 0 other;

alignment_scores:
  Quality: 41.00 Length: 16
  Ratio: 3.154 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 56.250

alignment_block:
US-09-485-529-104 x AA253179 ..
Align seg 1/1 to: AA253179 from: 1 to: 1521

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
||||:|||| |:::::||||| ::|||::|
181 GAAGTCTGCACAAATTGGGCTTTAAAGTTTCGGTTCGGATCAGCGC 228

seq_name: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT:AA253180

seq_documentation_block:
ID AA253180 standard; DNA; 1521 BP.
XX
AC AA253180;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 092 partial DNA sequence SEQ ID NO:311.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 02-SEP-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX
PI Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;
PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
PI Tettelin H, Venter JC;
XX
DR WPI; 2000-062150/05.

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DR P-PSDB; AA254418.
XX
PT Novel Neisseria meningitidis predicted to be useful antigens for
XX vaccines and diagnostics
XX
PS Claim 7; Page 289; 1453pp; English.
XX
CC AA253015 to AA254536, AA254577 to AA254615, and AA254615 to AA254615, and AA254615 to AA254615
CC represent novel Neisseria meningitidis and N. gonorrhoeae polynucleotides
CC and polypeptides. AA254537 to AA254576 and AA254616 to AA254616 to AA254616 to AA254616
CC PCR primers used in the exemplification of the present invention. The
CC polypeptides, the polynucleotides, antibodies and compositions of
CC the invention can be used as vaccines, as diagnostic reagents, and as
CC immunogenic compositions. The polypeptides can be used in the
CC manufacture of medicaments for treating or preventing infection due to
CC Neisseria meningitidis (e.g. meningitis and septicemia), to detect the
CC presence of Neisseria meningitidis, or to raise antibodies. They may also
CC be used to screen for agonists or antagonists, which may themselves
CC have use as antibacterial agents. The polynucleotides of the invention
CC may also be used in gene therapy protocols.
XX
SQ Sequence 1521 BP; 352 A; 444 C; 396 G; 329 T; 0 other;

alignment_scores:
  Quality: 41.00 Length: 16
  Ratio: 3.154 Gaps: 0
Percent Similarity: 81.250 Percent Identity: 56.250

alignment_block:
US-09-485-529-104 x AA253180 ..
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2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
||||:|||| |:::::||||| ::|||::|
181 GAAGTCTGCACAAATTGGGCTTTAAAGTTTCGGTTCGGATCAGCGC 228

seq_name: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT:AA253181

seq_documentation_block:
ID AA253181 standard; DNA; 1521 BP.
XX
AC AA253181;
XX
DT 21-MAR-2000 (first entry)
XX
DE Neisseria meningitidis ORF 092 partial DNA sequence SEQ ID NO:313.
XX
KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
KW antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;
KW antibacterial; gene therapy; ds.
XX
OS Neisseria meningitidis.
XX
PN WO9957280-A2.
XX
PD 11-NOV-1999.
XX
PF 30-APR-1999; 99WO-US09346.
XX
PR 01-MAY-1998; 98US-0083758.
PR 31-JUL-1998; 98US-0094869.
PR 02-SEP-1998; 98US-0098994.
PR 02-SEP-1998; 98US-0099062.
PR 02-SEP-1998; 98US-0103749.
PR 09-OCT-1998; 98US-0103794.
PR 09-OCT-1998; 98US-0103796.
PR 25-FEB-1999; 99US-0121528.
XX
PA (CHIR ) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
XX

```

PI Fraser C, Galeotti C, Grandi G, Hickey E, Masignani V, Mora M;
 PI Petersen J, Pizsa M, Rappuoli R, Ratti G, Scalato E, Scarselli M;
 PI Tettelin H, Venter JC;
 XX
 DR WPI: 2000-062150/05.
 DR P-PSDB; AAY74419.
 XX
 PT Novel Neisserial polypeptides predicted to be useful antigens for
 PT vaccines and diagnostics -
 XX
 PS Claim 7; Page 290-291; 1453pp; English.
 XX
 CC AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAZ74253 to AAY75941
 CC represent novel Neisseria meningitis and N. gonorrhoeae polynucleotides
 CC and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent
 CC PCR primers used in the exemplification of the present invention. The
 CC polypeptides, the polynucleotides, antibodies and compositions of
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medicaments for treating or preventing infection due to
 CC Neisserial bacteria (e.g. meningitis and septicemia), to detect the
 CC presence of Neisseria bacteria, or to raise antibodies. They may also
 CC be used to screen for agonists or antagonists, which may themselves
 CC have use as antibacterial agents. The polynucleotides of the invention
 CC may also be used in gene therapy protocols.
 XX
 SQ Sequence 1521 BP; 353 A; 436 C; 397 G; 335 T; 0 other;

alignment_scores:
 Quality: 41.00 Length: 16
 Ratio: 3.154 Gaps: 0
 Percent Similarity: 81.250 Percent Identity: 56.250
 alignment_block:
 US-09-485-529-104 x AAZ53181 ..
 Align seg 1/1 to: AAZ53181 from: 1 to: 1521
 2 GluteuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
 |||:::||||| |||||:::||||| :::|||||:::|||||
 181 GAAGCTGTGCACATTTGGGTTTAAAGTTTCCGGTTCGGATCAGGCG 228

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ71977
 seq_documentation_block:
 ID AAQ71977 standard; DNA; 1608 BP.

XX AAQ71977;
 AC
 XX
 XX 03-MAY-1995 (first entry)
 XX
 DE Murine IL-2R gamma gene.
 XX
 KW Murine IL2-R gamma; X-linked severe combined immunodeficiency;
 KW XSCID; interleukin; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 25..1134
 FT /*tag= a
 FT /transl_except= pos:1015..1017, aa:His
 FT sig_peptide 25..82
 FT /*tag= b
 FT /note= "Putative"
 FT
 XX
 XX WO9420641-A.
 XX
 XX 15-SEP-1994.
 PD
 XX
 XX 10-MAR-1994; 94WO-US02891.
 XX

PR 12-MAR-1993; 93US-0031143.
 PR 14-SEP-1993; 93US-0121435.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Leonard WJ, McBride WO, Noguchi M;
 XX
 DR WPI; 1994-303046/37.
 DR P-PSDB; AAR59094.
 XX
 PT Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
 PT comprises detecting mutated IL-2R gamma gene, also vectors and
 PT transgenic animals containing the mutated gene
 XX
 PS Example 1; Fig 7; 98pp; English.
 XX
 CC AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094,
 CC this was used in the development of a claimed method for the
 CC diagnosis of X-linked severe combined immunodeficiency (XSCID),
 CC in female carriers and male sufferers.
 XX
 SQ Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;
 alignment_scores:
 Quality: 41.00 Length: 13
 Ratio: 3.727 Gaps: 0
 Percent Similarity: 84.615 Percent Identity: 69.231
 alignment_block:
 US-09-485-529-104 x AAQ71977/rev ..
 Align seg 1/1 to reverse of: AAQ71977 from: 1 to: 1608
 2 GluteuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
 ||||| |||:::|||||:::||||| |||
 1409 GAGCTCCAGCACCCCTGGCTACAGGTAAGACTCTCT 1371
 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS06754
 seq_documentation_block:
 ID AAS06754 standard; cDNA; 2730 BP.
 XX
 AC AAS06754;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #54.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200138503-A2.
 PN
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US32085.
 XX
 XX 24-NOV-1999; 99US-0167482.
 PR
 PA (SUGE-) SUGEN INC.
 XX
 XX Plozman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 DR WPI; 2001-343950/36.
 DR P-PSDB; AAU03554.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing

OM of: US-09-485-529-104 to: EST:* out_format : pfs

Date: Dec 19, 2001 10:52 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-O=/cgn2_1/USPTO_spool/US09485529/runat_19122001_165004_14330/app_query.fasta_1.77
-DB=EST -QFWT=fastap -SUFFIX=p2n.rst -CAPOP=12.000 -GAPEXT=4.000
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-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPOP=7.000 -XGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossum62 -TRANS=human40.cdi
-LIST=1000 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=50 -MODE=LOCAL -OUTFWT=pfs -NORM=ext -MINLEN=0
-MAXLEN=2000000000 -USER=US09485529 -CGNI_1_3112 -NCPU=6
-TCPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-485-529-104

Query length: 17

Database: EST:*

Database sequences: 11351937

Database length: 1077921985

Search time (sec): 1381.990000

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gb_est2:BP268018	+	81.00	253.79	5.7e-05	844	BF268018 HV_CBA0019U17f Hordeum
gb_est2:BP39460	+	78.00	254.30	5.3e-05	263	B39460 RICS0803A Rice shoot Ory
gb_est1:AV410222	+	78.00	251.63	7.5e-05	355	AV410222 AV410222 Lotus japonic
gb_est1:BB321891	+	78.00	251.21	7.9e-05	372	BE321891 NF045007INIF1058 Insec
gb_est2:CP27475	+	78.00	250.84	8.3e-05	388	C27475 C27475 Rice callus cdna
gb_est1:AL363957	+	78.00	250.59	8.6e-05	399	AL363957 MTBA30809F1 MEBA Media
gb_est1:AU091413	+	78.00	250.59	8.6e-05	399	AU091413 AU091413 Rice cdna frc
gb_est1:AL369482	+	78.00	249.36	0.0001	458	AL369482 MTBA31006F1 MEBA Media
gb_est1:AL371425	+	78.00	249.21	0.0001	466	AL371425 MTBA44805F1 MEBA Media
gb_est1:AV422153	+	78.00	249.19	0.0001	467	AU422153 AV422153 Rice shoot Ory
gb_est1:AV422153	+	78.00	248.87	0.0001	484	AV422153 AV422153 Lotus japonic
gb_est1:AW695914	+	78.00	247.95	0.0001	537	AW695914 NF099H09STIF1079 Devel
gb_est1:AW695914	+	78.00	247.95	0.0001	559	AW695914 NF099H09STIF1079 Devel
gb_est2:BP308816	+	78.00	246.76	0.0001	614	BP308816 EST530226 GP0D Medicag
gb_est1:AW694061	+	78.00	246.18	0.0002	655	AW694061 NF072A05STIF1036 Devel
gb_est1:AW694061	+	78.00	246.17	0.0002	656	AW694061 NF072A05STIF1036 Devel
gb_est1:AW694061	+	78.00	246.02	0.0002	667	AW694061 NF107A12STIF1088 Devel
gb_est1:AW584593	+	78.00	245.81	0.0002	683	AW584593 N210669e MHAM Medicag
gb_est1:AW584593	+	78.00	245.58	0.0002	701	AW584593 N210669e MHAM Medicag
gb_est1:AA660952	+	78.00	245.35	0.0002	719	AA660952 00849 MKRHE Medicag
gb_est2:BG647068	+	78.00	245.00	0.0002	748	BG647068 EST508687 HOGA Medicag
gb_est2:BG440209	+	74.00	232.65	0.0009	684	BG440209 GA_Ea0006G06f Gossyp
gb_est1:AW584431	+	74.00	232.30	0.0009	712	AW584431 N210477e MHAM Medicag
gb_est1:AW688657	+	72.00	226.52	0.0012	651	AW688657 NF010B04STIF1000 Devel
gb_est1:AW495884	+	71.00	229.81	0.0012	311	AW495884 sb17d07.y1 Lotu-c1004 Gl
gb_est1:AV409731	+	71.00	228.38	0.0015	365	AV409731 AV409731 Lotus japonic
gb_est1:BB659954	+	71.00	226.42	0.0019	455	BB659954 746 GmaxSC Glycine ma
gb_est2:BP424878	+	71.00	226.23	0.0019	465	BP424878 su52b08.y1 Gm-c1069 Gl
gb_est1:AW720697	+	71.00	225.98	0.0020	478	AW720697 LJNEST7h8c Lotus jap
gb_est2:BP419686	+	71.00	224.17	0.0025	586	BP419686 LJNEST7h8c Lotus jap
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gb_est2:BP22782	+	70.00	223.10	0.0029	457	BP22782 4790 Lambda-PRL2 Arabid
gb_est1:AV526467	+	70.00	221.53	0.0036	545	AV526467 AV526467 Arabidopsis d
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gb_est1:AL371416	+	68.00	217.75	0.0058	398	AL371416 MTBA44805F1 MEBA Media
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gb_est1:BE202661	+	68.00	216.05	0.0072	482	BE202661 EST402683 KV1 Medic
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gb_est1:AW684591	+	68.00	214.98	0.0082	544	AW684591 NF018F10NRIF1000 No
gb_est1:AW693047	+	68.00	214.90	0.0082	601	AW693047 NF059C03STIF1020 De
gb_est1:AW697328	+	68.00	213.91	0.0094	613	AW697328 NF031E08STIF1086 De
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gb_est1:AW688696	+	68.00	213.45	0.0101	646	AW688696 NF018E08STIF1000 De
gb_est2:BG586532	+	68.00	213.38	0.0101	651	BG586532 EST488300 MHAM Medi
gb_est1:AW688030	+	68.00	213.31	0.0102	656	AW688030 NF003E05STIF1000 De
gb_est1:AW691058	+	68.00	213.31	0.0102	656	AW691058 NF040G10STIF1000 De
gb_est2:BP642607	+	68.00	213.30	0.0102	657	BP642607 NF063C08INIF1056 In
gb_est1:AW688198	+	68.00	213.28	0.0102	658	AW688198 NF004E08STIF1000 De
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gb_est2:BG644975	+	68.00	213.27	0.0103	659	BG644975 EST506594 KV3 Medic
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gb_est2:BG457232	+	68.00	213.23	0.0103	662	BG457232 NF101B04PLIF1031 Ph
gb_est2:BP263811	+	68.00	212.93	0.0107	685	BP263811 NF107A08PLIF1065 Ph
gb_est2:BG646792	+	68.00	212.66	0.0111	706	BG646792 EST508411 HOGA Medi
gb_est1:AV527188	+	68.00	212.43	0.0114	724	AV527188 AV527188 Arabidopsi
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gb_est2:BP4149902	+	60.00	189.33	0.0623	506	BP4149902 LJNEST94r Lotus ja
gb_est2:BP003233	+	54.00	171.51	2.17	409	BP003233 EST431661 KV1 Medic
gb_est1:AW719659	+	51.00	167.67	3.56	208	AW719659 LJNEST7h8r Lotus ja
gb_est2:BP370081	+	50.00	156.82	14.31	487	BP370081 RC5-FN0022-030800-0
gb_est1:AU083835	+	50.00	156.67	14.58	495	AU083835 AU083835 Cryptomeri
gb_est1:AV236965	+	49.00	160.28	9.18	228	AV236965 AV236965 RIKEN full
gb_est1:AV228139	+	49.00	159.86	9.68	239	AV228139 AV228139 RIKEN full
gb_est1:AA200022	+	49.00	156.32	15.26	356	AA200022 mu02802.r1 Soares m
gb_est1:AA200022	+	49.00	155.90	16.09	373	AA200022 mu02802.r1 Soares m
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gb_gss:AZ5086914	+	49.00	152.31	25.52	559	AZ5086914 RPCI-23-467N1.TV R
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gb_est1:BB101992	+	47.00	151.95	26.73	278	BB101992 BB101992 RIKEN full
gb_gss:CNS00TR3	+	47.00	150.29	33.06	335	AL090045 Arabidopsis thalian
gb_gss:CNS0215	+	47.00	139.73	128.03	1098	B09215 TB5-17 TAMU Arabido
gb_est1:BB162052	+	46.00	147.08	49.88	332	BB162052 BB162052 RIKEN full
gb_est1:AV340529	+	45.00	145.67	59.80	269	AV340529 AV340529 RIKEN full
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gb_gss:AZ299014	+	45.00	140.88	110.54	461	BE100587 UI-R-BJ1-atw-b-07-0
gb_gss:AZ299014	+	45.00	139.55	130.99	535	AZ299014 RPCI-23-119N13.TV R
gb_est1:BB176997	+	44.00	142.02	95.40	280	BB176997 BB176997 RIKEN full
gb_est1:BB320547	+	44.00	142.02	107.15	310	BB320547 BB320547 RIKEN full
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gb_est1:AL178063	+	44.00	139.69	128.68	364	AL178063 EST221722 Normalize
gb_est1:AL408207	+	44.00	139.19	137.18	385	AL408207 EST236497 Normalize
gb_est1:AW914911	+	44.00	138.94	141.66	396	AW914911 EST346215 Normalize
gb_est1:AL122811	+	44.00	138.88	142.89	399	AL122811 EST224806 Normalize
gb_est1:AA132459	+	44.00	138.53	149.03	414	AA132459 z007g09.s1 Stratage
gb_est2:W31487	+	44.00	138.23	155.20	429	W31487 zb29205.r1 Soares par
gb_est1:AL012448	+	44.00	138.15	156.85	433	AL012448 EST206899 Normalize
gb_est1:AL408211	+	44.00	137.64	167.64	459	AL408211 EST236501 Normalize
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gb_est2:BP286110	+	44.00	137.03	181.03	491	BP286110 UI-R-DDO-bzt-f-10-0
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gb_est1:BB660115	+	44.00	135.47	221.06	585	BB660115 674 GmaxSC Glycine
gb_gss:CNS02G3W	+	44.00	134.91	237.51	623	BF370111 RC5-FN0022-130600-0
gb_est2:BP370111	+	44.00	134.91	237.51	657	BF370111 RC5-FN0022-130600-0
gb_est2:BG069108	+	44.00	133.44	286.80	735	BG069108 H3072G11-3 NIA Mous
gb_gss:CNS03KRV	+	44.00	132.05	343.06	860	AL248548 Tetraodon nigroviri

gb_estl1:AV249715	112.74	140.72	43.00	102.44	112.74	224	AV249715	AV249715	RIXEN full-1e	gb_estl1:BB164856	391.93	131.01	41.00	102.44	391.93	319	BB164856	BB164856	RIXEN full
gb_estl1:AV249715	180.23	137.06	43.00	137.06	180.23	338	AV249715	EST270376	Schistosoma	gb_estl1:AV145474	396.13	130.92	41.00	130.92	396.13	322	AV145474	AV145474	Mus muscul
gb_estl1:BF370117	239.06	134.86	43.00	134.86	239.06	433	BF370117	RC5-FN0022	270700-Q33	gb_estl1:BB164625	406.33	130.84	41.00	130.84	406.33	325	BB164625	BB164625	RIXEN full
gb_gss:AZ221263	246.63	134.62	43.00	134.62	246.63	445	AZ221263	Gm.ISB001.005	D04.F.IS	gb_estl1:BB166530	418.66	130.49	41.00	130.49	418.66	338	BB166530	BB166530	RIXEN full
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gb_gss:AZ3310975	266.32	134.02	43.00	134.02	266.32	476	AZ3310975	IM0026M07F	Mouse 10kb	gb_estl1:AW545573	438.49	130.13	41.00	130.13	438.49	352	AW545573	CO195C12-3	NIA Mous
gb_gss:AZ3011957	283.62	133.53	43.00	133.53	283.62	503	AZ3011957	Gm.ISB001.005	D04.F.IS	gb_gss:AZ017359	471.32	129.57	41.00	129.57	471.32	375	AQ107359	HS-3105-B2	E03.W7C
gb_estl1:BE515841	327.09	132.42	43.00	132.42	327.09	570	BE515841	WHE0606E	E03.1062A	gb_estl1:AA940224	481.36	129.41	41.00	129.41	481.36	382	AQ40224	Y29B01.r1	Soares M
gb_gss:FR0033459	354.72	131.79	43.00	131.79	354.72	612	FR0033459	601342221F1	NIH.MGC.53	gb_estl1:AA941485	502.98	129.06	41.00	129.06	502.98	397	AA941485	IA90H10.r1	Melton M
gb_estl1:BE1103199	444.58	130.03	43.00	130.03	444.58	746	BE1103199	Fugu.rubripes	GSS sequ	gb_estl1:BBF61888	518.90	128.82	41.00	128.82	518.90	408	BBF61888	maa74F01.Y1	Soares
gb_estl1:BE195219	462.97	129.71	43.00	129.71	462.97	773	BE195219	60159248F1	NIH.MGC.7	gb_estl1:BG090584	526.16	128.71	41.00	128.71	526.16	413	BG090584	mac13407.Y1	Soares
gb_estl1:BG121621	465.02	129.67	43.00	129.67	465.02	776	BG121621	602351578F1	NIH.MGC.90	gb_estl1:AA260777	527.82	128.69	41.00	128.69	527.82	414	AA260777	va02B04.r1	Soares m
gb_estl1:BF787948	547.19	128.41	43.00	128.41	547.19	895	BF787948	60213140F1	NCI.CGAP.K	gb_estl1:AA114068	533.43	128.60	41.00	128.60	533.43	418	AA114068	AF114068	Homo sapie
gb_gss:CN505758	560.46	128.22	43.00	128.22	560.46	914	CN505758	Tetradon.nigroviridis		gb_estl1:BF881436	552.39	128.33	41.00	128.33	552.39	431	BF881436	QVI-EF0183	-031200-5
gb_estl1:BE79482	568.16	128.11	43.00	128.11	568.16	925	BE79482	60104905F1	NCI.CGAP.C	gb_estl1:AA509892	564.10	128.17	41.00	128.17	564.10	439	AA509892	vh51f05.r1	Soares_m
gb_estl1:BE782991	611.08	127.54	43.00	127.54	611.08	986	BE782991	601472244F1	NIH.MGC.67	gb_estl1:BG090982	567.04	128.13	41.00	128.13	567.04	441	BG090982	TaR1107E07F	TaR1
gb_estl1:BG176581	723.96	126.22	43.00	126.22	723.96	1144	BG176581	602313155F1	NIH.MGC.8	gb_estl1:BG091376	569.97	128.09	41.00	128.09	569.97	443	BG091376	mac15407.Y1	Soares
gb_hcc:AK014938	121.91	138.04	43.00	121.91	138.04	1858	AK014938	Mus musculus	adult ma	gb_estl1:BE200503	572.90	128.05	41.00	128.05	572.90	445	BE200503	ug63H11.x1	Soares_m
gb_hcc:AK014886	120.44	137.06	43.00	120.44	137.06	2191	AK014886	Mus musculus	adult ma	gb_estl1:BE200503	572.90	128.05	41.00	128.05	572.90	445	BE200503	ug63H11.x1	Soares_m
gb_gss:AZ827587	144.61	144.61	42.00	144.61	144.61	100	AZ827587	2M0104C09F	Mouse 10kb	gb_estl1:BBG141456	608.27	127.58	41.00	127.58	608.27	459	BBG141456	IA90H10.r1	Melton M
gb_estl1:BG222339	142.07	142.07	42.00	142.07	142.07	133	BG222339	na153H11.x1	NCI.CGAP.H	gb_estl1:BE456505	615.68	127.49	41.00	127.49	615.68	474	BE456505	ut09G11.x1	Soares_t
gb_estl1:BG222578	145.40	140.54	42.00	140.54	145.40	158	BG222578	na175G11.x1	NCI.CGAP.H	gb_estl1:BE332239	632.00	127.28	41.00	127.28	632.00	485	BE332239	ut09G11.x1	Soares_t
gb_gss:AZ312038	185.01	136.86	42.00	136.86	185.01	239	AZ312038	IM0027N12F	Stratagene	gb_gss:AZ819366	655.83	126.99	41.00	126.99	655.83	501	AZ819366	2M008N23R	Mouse 10
gb_estl1:BB399796	199.20	136.28	42.00	136.28	199.20	255	BB399796	BB399796	RIXEN full-1e	gb_gss:AZ819366	655.83	126.99	41.00	126.99	655.83	501	AZ819366	2M008N23R	Mouse 10
gb_estl1:BB399796	217.11	135.61	42.00	135.61	217.11	275	BB399796	AU179507	Medaka liver	gb_gss:AA274104	714.36	126.33	41.00	126.33	714.36	539	AA274104	v952H01.r1	Soares_m
gb_estl1:BB399796	258.07	134.27	42.00	134.27	258.07	320	BB399796	AU179507	Medaka liver	gb_estl1:AA274104	714.36	126.33	41.00	126.33	714.36	539	AA274104	v952H01.r1	Soares_m
gb_estl1:BB399796	282.12	133.29	42.00	133.29	282.12	346	BB399796	uv02B01.Y1	Soares_mous	gb_gss:AZ272504	726.45	126.07	41.00	126.07	726.45	548	AZ272504	IM0124H21F	Mouse 10
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares
gb_estl1:BB399796	292.37	133.29	42.00	133.29	292.37	357	BB399796	v122B01.Y1	Stratagene	gb_estl1:BG143464	738.55	126.07	41.00	126.07	738.55	556	BG143464	mba56D10.x1	Soares

gb_est1:B5629895	40.00	125.69	775.41	401	1	BEG29895	uu36c09.x1 Soares_mamm	gb_gss:CNS07488	-	40.00	118.71	1.9e+03	879
gb_est2:B660695	40.00	125.67	777.62	402	1	BEG29895	TgEsty15e10.y1 TgVed	gb_est2:BF232620	1.9e+03	40.00	118.54	1.9e+03	896
gb_est3:B6984221	40.00	125.47	797.50	411	1	BG984221	PMO-CN0150-200301-008	gb_est2:BG527856	2.0e+03	40.00	118.49	2.0e+03	901
gb_est1:AA142418	40.00	125.43	801.93	413	1	AA142418	ms0804.r1 Stratagene	gb_est2:BE969195	2.0e+03	40.00	118.39	2.0e+03	911
gb_est2:W96848	40.00	125.43	801.93	413	1	W96848	mf95c05.r1 Soares mouse	gb_gss:CNS06E9D	2.1e+03	40.00	118.05	2.1e+03	947
gb_est1:AV162063	40.00	125.40	804.14	414	1	AV162063	AV162063	gb_gss:CNS07590	2.1e+03	40.00	117.78	2.1e+03	976
gb_est1:A1772824	40.00	125.28	817.45	420	1	A1772824	EST253924 Tomato resis	gb_gss:CNS05IN58	2.4e+03	40.00	116.78	2.4e+03	1039
gb_est2:BG660362	40.00	125.21	824.11	423	1	BG660362	TgEsty407a02.y1 TgVed	gb_hlc:AK003IN9	3.1e+03	40.00	114.83	3.1e+03	1359
gb_est2:BF557639	40.00	125.17	825.56	425	1	BF557639	UI-R-CO-bx-a-07-0-UI-R	gb_hlc:AK008870	4.00	40.00	112.31	4.3e+03	1806
gb_est2:T27048	40.00	124.92	855.29	437	1	T27048	NIBT219C09R Infant brain	gb_est2:BF785554	39.50	40.00	116.63	2.5e+03	923
gb_est2:BG333690	40.00	124.84	864.22	441	1	BG333690	OVI_L6_D06-bl.A002 Ova	gb_est1:AA080759	39.00	40.00	128.41	546.77	204
gb_est2:BG993104	40.00	124.78	870.93	444	1	BG993104	RC4-H51109-0620201-014	gb_est1:AA1436954	39.00	40.00	128.24	559.02	208
gb_gss:AO682893	40.00	124.74	875.41	446	1	AO682893	HS-2229-B1_C03 SP6E RF	gb_est1:AW121277	39.00	40.00	126.75	676.91	246
gb_est1:BE162592	40.00	124.70	879.89	448	1	BE162592	PM1-HF0452-150300-004	gb_est1:AW404912	39.00	40.00	126.64	686.33	249
gb_est2:T86731	40.00	124.60	891.09	453	1	T86731	vd77f05.x1 Soares fetal	gb_est1:AV257911	39.00	40.00	126.53	695.77	252
gb_est2:BF151780	40.00	124.60	891.09	453	1	BF151780	uz20c11.y1 NCI_CGAP_Ma	gb_gss:BH035748	39.00	40.00	126.50	698.92	253
gb_gss:AZA2421997	40.00	124.43	911.31	462	1	AZ241997	IM0200E08F Mouse 10kb	gb_gss:BH0350022	39.00	40.00	126.50	698.92	253
gb_est2:BG904251	40.00	124.28	929.33	470	1	BG904251	TaLr1102F05F TaLr1 Tr1	gb_est1:AA917391	39.00	40.00	125.99	746.37	268
gb_est1:AW824521	40.00	124.22	936.10	473	1	AW824521	us10612.x1 Soares_NMGH	gb_est2:D24394	39.00	40.00	125.69	775.03	277
gb_gss:AZ825888	40.00	124.05	956.44	482	1	AZ825888	2M0101N13F Mouse 10kb	gb_est1:BB516804	39.00	40.00	125.19	826.28	293
gb_gss:AO502963	40.00	123.92	972.30	489	1	AO502963	V47C6 mtn-3xHA/lacZ In	gb_est1:BB286985	39.00	40.00	125.31	813.43	289
gb_est1:AA646019	40.00	123.89	976.83	491	1	AA646019	v829412.r1 Stratagene	gb_est1:AA050782	39.00	40.00	125.28	816.64	290
gb_est1:AA880174	40.00	123.85	981.37	493	1	AA880174	vv97g06.r1 Soares_mamm	gb_est1:BB516804	39.00	40.00	125.19	826.28	293
gb_est1:AA2673496	40.00	123.82	985.91	495	1	AA2673496	vr32c05.r1 Barstead mc	gb_gss:AO605631	39.00	40.00	125.07	839.16	297
gb_est1:AA270703	40.00	123.78	990.46	497	1	AA270703	va67b05.r1 Soares_mous	gb_gss:BE706303	39.00	40.00	124.92	855.29	302
gb_est1:AW908843	40.00	123.55	1.0e+03	510	1	AW908843	uf38c01.x1 Soares_mamm	gb_gss:AZ285604	39.00	40.00	124.66	881.18	310
gb_est1:AI649652	40.00	123.46	1.0e+03	515	1	AI649652	48607C12.y1 486 - les	gb_est1:AW851095	39.00	40.00	124.66	881.18	310
gb_gss:TA137804P	40.00	123.33	1.0e+03	523	1	AL65954	T. brucei sheared genc	gb_est2:BE933120	39.00	40.00	124.63	887.67	312
gb_est1:AA685564	40.00	123.28	1.1e+03	526	1	AA685564	vul7b12.r1 Barstead mc	gb_gss:CNS00W08	39.00	40.00	124.44	910.41	319
gb_est1:AW753318	40.00	123.19	1.1e+03	531	1	AW753318	RC5-C0254-031099-011	gb_est2:BE9599140	39.00	40.00	124.38	916.93	321
gb_est1:BB433359	40.00	123.12	1.1e+03	535	1	BB433359	EST399888 Tomato break	gb_est1:AA431598	39.00	40.00	124.33	923.44	323
gb_est2:BF470480	40.00	123.11	1.1e+03	536	1	BF470480	UI-M-BH3-av1-h-12-0-UI	gb_gss:AO421579	39.00	40.00	124.13	946.30	331
gb_est1:AI875584	40.00	123.09	1.1e+03	537	1	AI875584	uk50b05.x1 Sugano_mous	gb_est1:AW175826	39.00	40.00	124.11	949.57	331
gb_est1:AW744749	40.00	123.03	1.1e+03	541	1	AW744749	vr33a08.x1 Soares_mous	gb_est1:BE706286	39.00	40.00	124.03	959.40	334
gb_est1:BE626837	40.00	123.01	1.1e+03	542	1	BE626837	ut85a05.x1 Soares_mamm	gb_est1:AO032548	39.00	40.00	123.90	975.79	339
gb_est1:BE750188	40.00	123.01	1.1e+03	542	1	BE750188	201387 MARC 4BOV Bos t	gb_est1:AA431598	39.00	40.00	123.90	975.79	339
gb_est2:BG664529	40.00	122.96	1.2e+03	545	1	BG664529	DRABPA09 Rat DRG Bos t	gb_est1:BE770834	39.00	40.00	123.77	992.22	344
gb_est2:BG909314	40.00	122.89	1.1e+03	549	1	BG909314	TaLr1175H09F TaLr1 Tr1	gb_est1:AW608121	39.00	40.00	123.71	998.80	346
gb_est1:AI077307	40.00	122.77	1.1e+03	557	1	AI077307	Oy9q110.y1 Soares_feta	gb_est1:AW608121	39.00	40.00	123.71	998.80	346
gb_gss:AZ957674	40.00	122.75	1.1e+03	558	1	AZ957674	2M0224E08R Mouse 10kb	gb_est1:AU069744	39.00	40.00	123.66	1.0e+03	348
gb_est1:BI275683	40.00	122.56	1.2e+03	562	1	BI275683	606059G03.x2 606 - Ear	gb_gss:BB162825	39.00	40.00	123.59	1.0e+03	351
gb_est2:BG905794	40.00	122.56	1.2e+03	570	1	BG905794	TaLr1142E02F TaLr1 Tr1	gb_gss:AA042443	39.00	40.00	123.39	1.0e+03	359
gb_gss:AZA01890	40.00	122.55	1.2e+03	571	1	AZ01890	IM0168M19R Mouse 10kb	gb_est1:BI0347171	39.00	40.00	123.29	1.1e+03	363
gb_est1:AI179963	40.00	122.51	1.2e+03	573	1	AI179963	EST233694 Normalized r	gb_est2:H59004	39.00	40.00	123.12	1.1e+03	370
gb_est2:C87212	40.00	122.51	1.2e+03	573	1	C87212	C87212 C87212 Mouse fertili	gb_est1:BI271686	39.00	40.00	122.97	1.1e+03	376
gb_est1:AA516602	40.00	122.48	1.2e+03	575	1	AA516602	vh85E04.r1 Knowles Sol	gb_est1:AV687719	39.00	40.00	122.86	1.1e+03	381
gb_est2:C80683	40.00	122.34	1.2e+03	584	1	C80683	C80683 Mouse 3.5-dpc bla	gb_est1:AW126697	39.00	40.00	122.81	1.1e+03	383
gb_est1:BI275683	40.00	122.31	1.2e+03	586	1	BI275683	UI-R-CWO-bwm-e-01-0-UI	gb_est1:AO067962	39.00	40.00	122.76	1.1e+03	385
gb_est1:BE213409	40.00	122.15	1.2e+03	597	1	BE213409	EST0178 Triticum aesti	gb_est2:BI054971	39.00	40.00	122.67	1.1e+03	389
gb_gss:AZ2729595	40.00	121.99	1.2e+03	608	1	AZ2729595	RPCI-24-247D24.TJ RPCI	gb_gss:BO025381	39.00	40.00	122.63	1.1e+03	391
gb_est2:BG712391	40.00	121.97	1.2e+03	609	1	BG712391	Pg1lp_pk014.n2 Normali	gb_est1:AI044824	39.00	40.00	122.51	1.2e+03	396
gb_est2:BF282278	40.00	121.97	1.2e+03	609	1	BF282278	EST446957 Rat Gene Ind	gb_est1:AL362566	39.00	40.00	122.42	1.2e+03	400
gb_est2:BG905660	40.00	121.94	1.3e+03	611	1	BG905660	TaLr1141D12F TaLr1 Tr1	gb_est2:BI010193	39.00	40.00	122.42	1.2e+03	400
gb_gss:AZA49229	40.00	121.91	1.3e+03	621	1	AZ49229	IM0247D32F Mouse 10kb	gb_est2:BI326047	39.00	40.00	122.42	1.2e+03	400
gb_gss:AZA797776	40.00	121.80	1.3e+03	631	1	AZ797776	HS_2161_B2_F02_T7C Cit	gb_est2:BF868886	39.00	40.00	122.34	1.2e+03	404
gb_gss:AZ358261	40.00	121.66	1.3e+03	635	1	AZ358261	IM0100C10R Mouse 10kb	gb_gss:AZ876463	39.00	40.00	122.31	1.2e+03	405
gb_gss:AZ096618	40.00	121.56	1.3e+03	638	1	AZ096618	RPCI-23-18B16.TJ RPCI	gb_est2:D24416	39.00	40.00	122.27	1.2e+03	407
gb_gss:AZ743492	40.00	121.54	1.3e+03	639	1	AZ743492	RPCI-24-14605.TJ RPCI	gb_est1:BI010193	39.00	40.00	122.14	1.2e+03	413
gb_est1:BI169746	40.00	121.45	1.3e+03	646	1	BI169746	EST125645 Normalized r	gb_est2:BF987917	39.00	40.00	122.03	1.2e+03	418
gb_est2:BF227152	40.00	121.39	1.3e+03	650	1	BF227152	uz20c11.x1 NCI_CGAP_Ma	gb_est2:BI054971	39.00	40.00	121.99	1.2e+03	420
gb_est1:AW112170	40.00	120.90	1.4e+03	687	1	AW112170	MC1248 mouse liver, ve	gb_est1:AA079387	39.00	40.00	121.97	1.2e+03	421
gb_est2:BG380739	40.00	120.81	1.4e+03	694	1	BG380739	UI-R-CWO-bua-h-04-0-UI	gb_est1:AA032661	39.00	40.00	121.95	1.2e+03	422
gb_est2:BF681905	40.00	120.67	1.5e+03	705	1	BF681905	602117052T1 Soares_mam	gb_gss:AZ358586	39.00	40.00	121.91	1.3e+03	424
gb_gss:AZ048210	40.00	120.66	1.5e+03	706	1	AZ048210	clm-c62-t clm Giardia	gb_est2:BI010193	39.00	40.00	121.84	1.3e+03	427
gb_gss:AZ0866030	40.00	120.60	1.5e+03	711	1	AZ0866030	2M0176E24F Mouse 10kb	gb_est1:AW010527	39.00	40.00	121.78	1.3e+03	430
gb_est2:BF865717	40.00	120.53	1.5e+03	716	1	BF865717	963061F09.x1 C. reinh	gb_est1:AA798691	39.00	40.00	121.76	1.3e+03	431
gb_est1:BI152260	40.00	120.51	1.5e+03	718	1	BI152260	602917676F1 NCI_CGAP	gb_est1:AA798691	39.00	40.00	121.72	1.3e+03	433
gb_gss:AZ751965	40.00	120.51	1.5e+03	718	1	AZ751965	RPCI-24-6663.TJ RPCI	gb_gss:AZ943980	39.00	40.00	121.62	1.3e+03	438
gb_est2:BF631442	40.00	119.78	1.7e+03	779	1	BF631442	HVSME0015P10F Hordcum	gb_est1:AI037267	39.00	40.00	121.60	1.3e+03	439
gb_gss:AZ7539165	40.00	119.60	1.7e+03	795	1	AZ7539165	602038470F1 NCI_CGAP	gb_gss:BI96566	39.00	40.00	121.54	1.3e+03	442
gb_est1:AL423934	40.00	118.98	1.7e+03	797	1	AL423934	TA_end of clone A02A0A	gb_est1:AI051194	39.00	40.00	121.44	1.3e+03	447
gb_est2:BF274326	40.00	118.58	1.8e+03	853	1	BF274326	GA_Eb02020L15f Gossyp	gb_est1:AW792896	39.00	40.00	121.38	1.3e+03	450

gb_estl1:AA636315	39.00	121.36	1.4e+03	451	AA636315	vg76el2.sl Knowles Sol	gb_est2:BG754881	39.00	118.33	2.0e+03	634	BG754881	602714270F1 NIH_MGC
gb_estl1:AA636315	39.00	121.36	1.4e+03	451	AA636315	hd12d09.x1 Soares_NFL	gb_est2:BG755970	39.00	118.31	2.0e+03	635	BG755970	602716448F1 NIH_MGC
gb_estl1:BF989547	39.00	121.34	1.4e+03	452	BF989547	CM3-GN092-201000-411	gb_est2:BG755976	39.00	118.31	2.0e+03	636	BG755976	EST491414 CSTS Sola
gb_gss:AA2364562	39.00	121.32	1.4e+03	453	AA2364562	IM0110E22R Mouse 10kb	gb_est2:BG592911	39.00	118.29	2.0e+03	637	BG592911	EST491589 CSTS Sola
gb_estl1:BF016508	39.00	121.32	1.4e+03	450	BF016508	uv37el2.sl NCI_CGAP_Lu	gb_hsc:AA012628	39.00	118.29	2.0e+03	637	AA012628	Mus musculus 10_11
gb_estl1:AA215645	39.00	121.16	1.4e+03	461	AA215645	zr98d08.sl NCI_CGAP_GC	gb_gss:AA022608	39.00	118.26	2.0e+03	639	AA022608	RPCI-23-385321.TJ R
gb_gss:AA2495813	39.00	121.05	1.4e+03	465	AA2495813	IM0333A21R Mouse 10kb	gb_est2:BG756047	39.00	118.25	2.0e+03	640	BG756047	602716538F1 NIH_MGC
gb_gss:AA2750989	39.00	121.05	1.4e+03	467	AA2750989	RPCI-24-66C9.TJ RPCI-2	gb_estl1:AA040966	39.00	118.23	2.0e+03	641	AA040966	DKFZP43412415_r1.43
gb_estl1:BF327045	39.00	121.03	1.4e+03	468	BF327045	RC2-BN0048-250400-018	gb_estl1:AA1663112	39.00	118.20	2.0e+03	643	AA1663112	uk22h05.y1 Sugano m
gb_estl1:BF369503	39.00	120.97	1.4e+03	471	BF369503	CM3-GN0092-160900-353	gb_estl1:BA1282272	39.00	118.16	2.0e+03	646	BA1282272	UI-R-CU05-cdy-f-04
gb_estl1:BF113719	39.00	120.86	1.4e+03	477	BF113719	ESW441309 tomato root.	gb_estl1:BF608468	39.00	118.08	2.1e+03	652	BF608468	MY1_001410 Mouse 9-
gb_estl1:AA763603	39.00	120.77	1.5e+03	481	AA763603	vg97a01.r1 Soares_mamm	gb_gss:AA259352	39.00	118.05	2.1e+03	654	AA259352	RPCI-23-218321.TV R
gb_gss:AA2085572	39.00	120.77	1.5e+03	482	AA2085572	RPCI-23-467121.TVB RPC	gb_estl1:AA6614595	39.00	117.98	2.1e+03	659	AA6614595	hno2b12.x1 NCI_CGAP
gb_gss:BA0815	39.00	120.67	1.5e+03	487	BA0815	1T9R8TF TAMU Arabidopsis	gb_gss:AA2340851	39.00	117.93	2.1e+03	663	AA2340851	IM0073A02F Mouse 10
gb_estl1:AA1625958	39.00	120.64	1.5e+03	489	AA1625958	vg97a01.r1 Soares_mamm	gb_estl1:BG595221	39.00	117.89	2.1e+03	666	BG595221	EST493899 CSTS Sola
gb_estl1:AA1143538	39.00	120.62	1.5e+03	490	AA1143538	qg90h05.sl Soares_tota	gb_estl1:BA1225739	39.00	117.89	2.1e+03	666	BA1225739	602951360F1 NIH_MGC
gb_estl1:AA280478	39.00	120.60	1.5e+03	491	AA280478	qg03a11.sl Soares_feta	gb_gss:AA280669	39.00	117.81	2.1e+03	672	AA280669	IM0336N05F Mouse 10
gb_estl1:AA1656364	39.00	120.58	1.5e+03	492	AA1656364	t445c01.x1 NCI_CGAP_GC	gb_estl1:BE513381	39.00	117.80	2.1e+03	673	BE513381	601315714F1 NIH_MGC
gb_estl1:BF141589	39.00	120.58	1.5e+03	492	BF141589	UI-R-CA0-bpb-e-02-0-UI	gb_gss:BA123408	39.00	117.78	2.1e+03	674	BA123408	RPCI-23-30G5.TV RPC
gb_estl1:BF919758	39.00	120.57	1.5e+03	493	BF919758	EST423527 potato leave	gb_gss:BA112592	39.00	117.77	2.1e+03	675	BA112592	RPCI-24-357K20.TV R
gb_estl1:BF892786	39.00	120.55	1.5e+03	494	BF892786	QV1-MT0132-081100-435	gb_estl1:BG396960	39.00	117.72	2.2e+03	679	BG396960	601290693F1 NIH_MGC
gb_estl1:BG600311	39.00	120.53	1.5e+03	495	BG600311	EST505206 CSTS Solanum	gb_gss:BA051901	39.00	117.69	2.2e+03	681	BA051901	RPCI-24-243G7.TJ RP
gb_gss:CNS00P7N	39.00	120.53	1.5e+03	495	CG00311	EST505206 CSTS Solanum	gb_estl1:BG593805	39.00	117.64	2.2e+03	685	BG593805	EST492483 CSTS Sola
gb_estl1:BF252195	39.00	120.49	1.5e+03	497	BF252195	UI-R-AB1-ys-f-04-0-UI	gb_estl1:BG810175	39.00	117.64	2.2e+03	685	BG810175	602332768F1 NIH_MGC
gb_estl1:BF151823	39.00	120.40	1.5e+03	502	BF151823	u220g12.y1 NCI_CGAP_Ma	gb_estl1:BE271378	39.00	117.60	2.2e+03	688	BE271378	601140260F1 NIH_MGC
gb_estl1:AA901534	39.00	120.40	1.5e+03	508	AA901534	NCM3HG73 Mycelial Neur	gb_estl1:BG761928	39.00	117.50	2.2e+03	696	BG761928	602718163F1 NIH_MGC
gb_gss:AA2498358	39.00	120.40	1.5e+03	513	AA2498358	IM0335C11R Mouse 10kb	gb_estl1:BE274165	39.00	117.46	2.2e+03	699	BE274165	601120708F1 NIH_MGC
gb_estl1:BF689522	39.00	120.21	1.6e+03	519	BF689522	602186902F1 NIH_MGC_4	gb_estl1:BG106604	39.00	117.45	2.2e+03	700	BG106604	602290427F1 NIH_MGC
gb_gss:AA244885	39.00	120.09	1.6e+03	520	AA244885	HS_2081.A2_F05_T7 CIT	gb_estl1:BG351411	39.00	117.40	2.2e+03	704	BG351411	108A01 Mature tuber
gb_estl1:BF653330	39.00	120.04	1.6e+03	523	BF653330	7H88C06.x1 NCI_CGAP_Cc	gb_estl1:BG595732	39.00	117.31	2.3e+03	711	BG595732	EST494410 CSTS Sola
gb_gss:AA0672393	39.00	120.01	1.6e+03	525	AA0672393	HS_2276.B2_D02_MR CIT	gb_estl1:BG597433	39.00	117.28	2.3e+03	713	BG597433	EST496111 CSTS Sola
gb_estl1:BF279498	39.00	119.97	1.6e+03	531	BF279498	bf301np.sl Neurospora	gb_estl1:BG747680	39.00	117.22	2.3e+03	718	BG747680	602222793F1 NCI_CGA
gb_estl1:BG134151	39.00	119.91	1.6e+03	531	BG134151	EST467043 tomato crown	gb_estl1:BE880130	39.00	117.17	2.3e+03	722	BE880130	601513109F1 NIH_MGC
gb_gss:AA24946975	39.00	119.91	1.6e+03	531	AA24946975	2M020F02F Mouse 10kb	gb_estl1:BG644038	39.00	116.94	2.4e+03	741	BG644038	EST512232 tomato sh
gb_estl1:BF34949	39.00	119.89	1.6e+03	532	BF34949	EST46027 tomato break	gb_estl1:BG831616	39.00	116.87	2.4e+03	747	BG831616	602763880F1 NIH_MGC
gb_estl1:AA210147	39.00	119.84	1.6e+03	535	AA210147	u151d09.y1 Rashbass K4	gb_gss:BA055190	39.00	116.79	2.4e+03	754	BA055190	RPCI-24-278G19.TV R
gb_estl1:BF634013	39.00	119.72	1.7e+03	542	BF634013	w332g05.y1 NCI_CGAP_K4	gb_estl1:BG740400	39.00	116.78	2.4e+03	755	BG740400	602764574F1 NIH_MGC
gb_estl1:AAW608735	39.00	119.72	1.7e+03	542	AAW608735	QV2-PW0012-010200-038	gb_estl1:BG599702	39.00	116.74	2.4e+03	758	BG599702	EST504597 CSTS Sola
gb_gss:AA2826794	39.00	119.72	1.7e+03	542	AA2826794	2M010211R Mouse 10kb	gb_estl1:BG596950	39.00	116.73	2.4e+03	759	BG596950	EST495628 CSTS Sola
gb_estl1:BF459825	39.00	119.67	1.7e+03	545	BF459825	065H06 Mature tuber la	gb_estl1:AAU122353	39.00	116.72	2.5e+03	760	AAU122353	AAU122353 MAMMAL Hom
gb_gss:AA2793772	39.00	119.63	1.7e+03	548	AA2793772	xm30a11.x1 NCI_CGAP_GC	gb_gss:BA086300	39.00	116.66	2.5e+03	765	BA086300	RPCI-24-310C22.TV R
gb_estl1:AA796415	39.00	119.58	1.7e+03	551	AA796415	wj17e10.x1 NCI_CGAP_K4	gb_gss:AA249195	39.00	116.64	2.5e+03	767	AA249195	T17N15-17 TAMU Arab
gb_estl1:BF892773	39.00	119.38	1.7e+03	563	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD Solanum	gb_estl1:BG820429	39.00	116.58	2.5e+03	772	BG820429	AU140804 PLACE4 Hom
gb_estl1:BF892773	39.00	119.37	1.7e+03	564	BF892773	EST515124 CSTD S							

gb_estl:BE054797	39.00	114.77	3.1e+03	946	BE054797	GA_Ea0031G19f	Gossyp	gb_est2:BF550641	38.00	119.36	1.7e+03	390	BF550641	UI-R-C0-hr-f-10-0-U
gb_est2:BE087162	39.00	114.77	3.1e+03	946	BI087162	602850842F1	NTH_MGC_10	gb_est2:TI18864	38.00	119.07	1.8e+03	403	TI18864	h06019t Testis.1 Homo
gb_estl:A535816	39.00	114.77	3.2e+03	952	AL535816	602535816	LTI_FL003_F8	gb_estl:AA965081	38.00	119.01	1.8e+03	406	AA965081	UI-R-C0-gz-b-03-0-U
gb_estl:A519809	39.00	114.57	3.2e+03	967	AL519809	AL519809	LTI_NFL004_NH	gb_estl:AW77964	38.00	118.94	1.8e+03	409	AW77964	f44204.0.Y1 Zebrafis
gb_est2:BE107106	39.00	114.37	3.3e+03	990	BG107106	602291010f1	NTH_MGC_8	gb_estl:AF114097	38.00	118.90	1.9e+03	411	AF114097	AF114097 Homo sapie
gb_gss:CN503PL4	39.00	114.06	3.4e+03	1025	AL254785	Tetraodon	NTH_MGC_8	gb_estl:AI1580407	38.00	118.88	1.9e+03	412	AI1580407	tm42H04.x1 NCI_CGAP
gb_est2:BF348255	39.00	113.83	3.6e+03	1052	BF348255	602027197f1	NCI_CGAP	gb_estl:AW405257	38.00	118.88	1.9e+03	412	AW405257	UI-HF-BK0-aas-f-02-
gb_est2:BF330867	39.00	113.73	3.6e+03	1063	BF330867	602072525f1	NCI_CGAP	gb_estl:AW478499	38.00	118.85	1.9e+03	413	AW478499	20541 MARC 1BOV Bos
gb_estl:BE040722	39.00	113.71	3.6e+03	1066	BE040722	OF05F06	OF Orviza satii	gb_estl:AW834878	38.00	118.79	1.9e+03	416	AW834878	RC6-LT0003-170100
gb_gss:CN503637	39.00	113.50	3.7e+03	1091	AL230114	Tetraodon	NTH_MGC_4	gb_estl:BE071782	38.00	118.79	1.9e+03	416	BE071782	RC6-BF0518-131299-0
gb_est2:BE033834	39.00	113.24	3.8e+03	1124	BG338340	602436120f1	NIH_MGC_4	gb_est2:R22298	38.00	118.77	1.9e+03	417	R22298	yh26a10.x1 Soares pia
gb_htc:AK00601	39.00	112.39	4.3e+03	1236	AK009601	Mus musculus	adult male	gb_estl:AI1819667	38.00	118.68	1.9e+03	421	AI1819667	wj59g02.x1 NCI_CGAP
gb_est2:BE0823596	39.00	111.16	5.0e+03	1420	BG823596	602728986f1	NIH_MGC_1	gb_estl:BE099237	38.00	118.68	1.9e+03	421	BE099237	UI-R-BJ1-atz-h-10-0
gb_htc:AK016037	39.00	110.97	5.1e+03	1450	AK016037	Mus musculus	adult male	gb_est2:BF474013	38.00	118.64	1.9e+03	423	BF474013	WHE0840.A04 B0825 W
gb_htc:AK016425	39.00	110.52	5.1e+03	1460	AK016425	Mus musculus	adult male	gb_est2:BF524582	38.00	118.64	1.9e+03	423	BF524582	UI-R-AA0-ws-g-10-0
gb_htc:BC009948	39.00	120.40	2.0e+04	4708	BC009948	Homo sapiens	clone	gb_estl:AV410098	38.00	118.56	1.9e+03	427	AV410098	AV410098 Lotus japo
gb_est2:BE0944378	38.50	124.72	878.43	257	BF944378	RC5-NN1164	-131000-011	gb_est2:R22298	38.00	118.47	2.0e+03	431	R22298	yh26a10.x1 Soares pia
gb_est2:BE0688489	38.50	119.52	1.7e+03	461	BG688489	336135	BARC 5BOV Bos t	gb_estl:AI1819667	38.00	118.68	1.9e+03	421	AI1819667	wj59g02.x1 NCI_CGAP
gb_estl:AW653600	38.50	118.15	2.0e+03	538	AW653600	102365	MARC 1BOV Bos t	gb_estl:BE099237	38.00	118.68	1.9e+03	421	BE099237	UI-R-BJ1-atz-h-10-0
gb_estl:BE258748	38.50	116.46	2.5e+03	650	BE258748	60113752f1	NTH_MGC_16	gb_est2:BF524968	38.00	118.43	2.0e+03	434	BF524968	UI-R-A0-af-c-06-0-U
gb_gss:AZ806213	38.00	130.22	433.44	115	AZ806213	2M0068C12F	Mouse 10kb	gb_est2:N76851	38.00	118.39	2.0e+03	435	N76851	vy48h02.r1 Soares fet
gb_estl:AA027541	38.00	128.60	533.61	138	AA027541	mi06a02	r1 Soares	gb_gss:AO686867	38.00	118.37	2.0e+03	436	AO686867	nbx0073019r CUGI R
gb_gss:AZ839001	38.00	128.10	569.03	146	AZ839001	2M0134124R	Mouse 10kb	gb_gss:AO706257	38.00	118.33	2.0e+03	438	AO706257	HS_3553.AL_E08.T7A
gb_estl:BE0339785	38.00	126.04	740.82	184	BE0339785	AB039785	Riken full-le	gb_est2:HB1045	38.00	118.17	2.0e+03	446	HB1045	yu60d03.s1 Soares fet
gb_estl:AV005499	38.00	125.57	786.91	194	AV005499	AB005499	Mus musculus	gb_gss:AO7371725	38.00	118.13	2.0e+03	448	AO7371725	HS_5380.B2_G04.SP6E
gb_estl:AI1050685	38.00	124.78	870.71	212	AI1050685	0V42C03	s1 Soares test	gb_estl:AI1704112	38.00	118.07	2.1e+03	451	AI1704112	UI-R-AF0-yc-e-12-0-
gb_est2:BG723352	38.00	124.02	960.25	231	BG723352	602694007f1	NTH_MGC_97	gb_est2:BI1005179	38.00	118.07	2.1e+03	451	BI1005179	PM3-HF0076-020401-0
gb_est2:BG772922	38.00	124.02	960.25	231	BG772922	602721152f1	NTH_MGC_97	gb_est2:N90464	38.00	118.05	2.1e+03	452	N90464	zai17c01.r1 Soares fet
gb_estl:AV431391	38.00	123.76	993.51	238	AV431391	AV431391	Poryphyra yezo	gb_estl:BN099910	38.00	118.01	2.1e+03	454	BN099910	UI-R-BJ1-atl-e-11-0
gb_estl:BA468954	38.00	123.21	1.1e+03	253	BA468954	BB468954	Riken full-le	gb_estl:BF453879	38.00	118.01	2.1e+03	454	BF453879	maa72h09.y1 Soares
gb_estl:AW341589	38.00	122.97	1.1e+03	260	AW341589	hd11f1.x1	Soares NFL	gb_estl:BF453879	38.00	118.01	2.1e+03	454	BF453879	maa72h09.y1 Soares
gb_est2:H33457	38.00	122.50	1.2e+03	274	H33457	EST109475	Rat PC-12 cell	gb_estl:AO507996	38.00	117.99	2.1e+03	455	AO507996	AL507996 Hordeum vu
gb_estl:AA860223	38.00	122.09	1.2e+03	287	AA860223	4k48e07	s1 Soares test	gb_estl:H20571	38.00	117.95	2.1e+03	457	H20571	ym47h08.s1 Soares inf
gb_estl:BF152845	38.00	121.94	1.3e+03	292	BF152845	uz96f12	y1 NCI_CGAP	gb_estl:AI158054	38.00	117.93	2.1e+03	458	AI158054	ud26d04.r1 Soares t
gb_estl:AV330198	38.00	121.91	1.3e+03	293	AV330198	AV330198	Riken full-le	gb_estl:AW531334	38.00	117.90	2.1e+03	460	AW531334	UI-R-BUO-ane-c-05-0
gb_estl:AA482568	38.00	121.88	1.3e+03	294	AA482568	zt34e08	s1 Soares ovan	gb_estl:BF931618	38.00	117.82	2.1e+03	464	BF931618	IL2-NT0203-141200-3
gb_estl:BB514566	38.00	121.85	1.3e+03	295	BB514566	BB514566	Riken full-le	gb_estl:AA549217	38.00	117.80	2.1e+03	466	AA549217	VK74F02.s1 Knowles
gb_estl:BB234757	38.00	121.79	1.3e+03	297	BB234757	BB234757	Riken full-le	gb_estl:BF32681	38.00	117.78	2.1e+03	466	BF32681	nael14a05.x1 NCI_CGA
gb_estl:BB006104	38.00	121.61	1.3e+03	302	BB006104	BB006104	Riken full-le	gb_gss:BF380257	38.00	117.76	2.1e+03	467	BF380257	UI-R-CS0-btq-h-03-0
gb_estl:BF232974	38.00	121.52	1.3e+03	306	BF232974	UI-R-YO-vg-g-07-0-U	UI-R	gb_gss:AO821719	38.00	117.74	2.1e+03	468	AO821719	HS_5431.A2.D03.SP6E
gb_estl:BF120203	38.00	121.32	1.4e+03	312	BF120203	UI-R-CA0-bap-g-05-0-U	UI-R	gb_gss:AO133855	38.00	117.74	2.1e+03	468	AO133855	HS_3075.A2.F03.MF C
gb_estl:BF881862	38.00	121.32	1.4e+03	313	BF881862	QV1-ET0181	-041200-550	gb_estl:AV641738	38.00	117.67	2.2e+03	472	AV641738	Chlamydomo
gb_estl:AA818078	38.00	121.26	1.4e+03	315	AA818078	UI-R-A0-ag-c-06-0-U	UI-R	gb_estl:AA624178	38.00	117.61	2.2e+03	475	AA624178	vm98a06.r1 Knowles
gb_estl:BG738088	38.00	121.23	1.4e+03	316	BG738088	fp04a02	s1 Zebrafis g	gb_gss:AZ493627	38.00	117.57	2.2e+03	477	AZ493627	AV639627 Chlamydomo
gb_estl:AV139804	38.00	121.12	1.4e+03	320	AV139804	AV139804	Mus musculus	gb_gss:AZ493627	38.00	117.50	2.2e+03	481	AZ493627	1M0328D06F Mouse 10
gb_estl:BF922588	38.00	121.12	1.4e+03	320	BF922588	QV4-1N0252	-191100-570	gb_estl:AW487740	38.00	117.48	2.2e+03	482	AW487740	89367 MARC 1BOV Bos
gb_estl:AW528494	38.00	121.10	1.4e+03	321	AW528494	UI-R-BT1-ako-r-08-0-U	UI-R	gb_estl:BF76562	38.00	117.46	2.2e+03	483	BF76562	287396 MARC 3BOV Bo
gb_gss:AZ067189	38.00	121.04	1.4e+03	323	AZ067189	RPCI-23-432M20	TJ RPCI	gb_gss:AO718264	38.00	117.44	2.2e+03	484	AO718264	HS_5513.B1.C06.T7A
gb_estl:TI90021	38.00	120.90	1.4e+03	328	TI90021	YQ38h08	s1 Soares fetal	gb_gss:AO134709	38.00	117.44	2.2e+03	484	AO134709	HS_3052.B1.C07.MF C
gb_estl:AI175238	38.00	120.88	1.4e+03	329	AI175238	UI-R-YO-vc-b-12-0-U	UI-R	AL426911	38.00	117.44	2.2e+03	484	AL426911	clone BA0AB015G12 o
gb_estl:BF164632	38.00	120.77	1.5e+03	333	BF164632	UI-R-YO-abw-c-04-0-U	UI-R	gb_estl:AA874831	38.00	117.41	2.2e+03	486	AA874831	UI-R-E0-cg-f-05-0-U
gb_estl:BF10563	38.00	120.74	1.5e+03	334	BF10563	NKSI_060	AI1_F NKSI (N	gb_estl:BF461085	38.00	117.41	2.2e+03	486	BF461085	UI-M-CGOp-bmk-g-08-
gb_estl:AW657690	38.00	120.66	1.5e+03	337	AW657690	tm81h10	s1 NCI_CGAP	gb_gss:AZ240206	38.00	117.28	2.3e+03	493	AZ240206	RPCI-23-71BA TJ RPC
gb_estl:AA860213	38.00	120.53	1.5e+03	342	AA860213	ak46d06	s1 Soares test	gb_estl:BE980908	38.00	117.17	2.3e+03	499	BE980908	UI-M-BH3-asw-b-03-0
gb_estl:AA883975	38.00	120.53	1.5e+03	342	AA883975	am27a04	s1 Soares NFL	gb_estl:AW789834	38.00	117.15	2.3e+03	500	AW789834	CO1365-F Lambda Zap
gb_estl:AI1563524	38.00	120.53	1.5e+03	342	AI1563524	EST00648	watermelon la	gb_estl:BE5474655	38.00	117.14	2.3e+03	501	BE5474655	sp66g11.y1 Gm-cl044
gb_estl:AW0807713	38.00	120.45	1.5e+03	344	AW0807713	xb68c11	x1 Soares NFL	gb_estl:BF558842	38.00	117.14	2.3e+03	501	BF558842	UI-R-AD-v-c-10-0-U
gb_estl:AI1479322	38.00	120.45	1.5e+03	345	AI1479322	tm27b07	x1 Soares NFL	gb_estl:BB662409	38.00	117.12	2.3e+03	503	BB662409	ST84/ST04G10 Pine T
gb_estl:BE0575905	38.00	120.35	1.5e+03	348	BE0575905	209786	MARC 2BOV Bos t	gb_estl:BE580142	38.00	117.08	2.3e+03	504	BE580142	uw13a05.y1 Soares m
gb_estl:AW141415	38.00	120.35	1.5e+03	349	AW141415	EST294441	Normalized r	gb_estl:AW494484	38.00	117.08	2.3e+03	504	AW494484	UI-M-BH3-aum-h-03-0
gb_estl:BE097046	38.00	120.28	1.6e+03	352	BE097046	UI-R-B01-apw-g-05-0-U	UI-R	gb_gss:AB074371	38.00	117.08	2.3e+03	504	AB074371	an36e12 JM101 filte
gb_estl:BF922137	38.00	120.13	1.6e+03	358	BF922137	CM2-NT0169	-181100-534	gb_gss:BBH073720	38.00	117.07	2.3e+03	505	BBH073720	RPCI-24-228F13 TJ R
gb_gss:AZ2945993	38.00	120.03	1.6e+03	362	AZ2945993	2M0207004R	Mouse 10kb	gb_estl:AA105958	38.00	117.00	2.4e+03	509	AA105958	ms84f09.r1 Soares m
gb_estl:AA494094	38.00	119.86	1.6e+03	369	AA494094	dg61f02	s1 NCI_CGAP	gb_estl:AW535928	38.00	117.00	2.4e+03	509	AW535928	UI-R-C4-amb-a-04-0
gb_gss:AOQ35495	38.00	119.76	1.7e+03	373	AOQ35495	CIT-HSP-2324F1	TF CIT	gb_estl:AA183880	38.00	116.96	2.4e+03	511	AA183880	mt21b04.r1 Soares m
gb_estl:AI145268	38.00	119.69	1.7e+03	376	AI145268	UI-R-BT0-qf-h-05-0-U	UI-R	gb_estl:BE8501922	38.00	116.93	2.4e+03	513	BE8501922	hm36h11.x1 NCI_CGAP
gb_gss:AZ608436	38.00	119.69	1.7e+03	376	AZ608436	1M0432C09R	Mouse 10kb	gb_gss:AZ851326	38.00	116.87	2.4e+03	516		

gb_gss:BH056025	38.00	116.67	2.5e+03	528	1	BH056025	RPCI-24-365A16.TJ.RPCI	gb_est2:BE898980	38.00	112.70	4.1e+03	825	1	BE898980	60151224LF1.NIH.MGC
gb_gss:Q772888	38.00	116.54	2.5e+03	533	1	Q772888	MS_2258.A2.P02.MR.CIT	gb_gss:AQ573945	38.00	112.63	4.1e+03	832	1	AQ573945	nbxb0083601f.CUGI.R
gb_est2:BF660799	38.00	116.54	2.5e+03	536	1	BF660799	msa72h09.x1.Soaress.mou	gb_est2:W08409	38.00	112.59	4.2e+03	835	1	W08409	mb49a10.x1.Soaress.mou
gb_gss:AZ382398	38.00	116.54	2.5e+03	536	1	AZ382398	1M0139L08R.Mouse.10kb	gb_est2:BG537584	38.00	112.56	4.2e+03	838	1	BG537584	602565916f1.NIH.MGC
gb_est1:AA967290	38.00	116.50	2.5e+03	538	1	AA967290	vz39h09.r1.Soaress.chym	gb_est1:AL3661129	38.00	112.52	4.2e+03	842	1	AL3661129	LTI.NFL010
gb_est2:C78770	38.00	116.50	2.5e+03	538	1	C78770	C78770.Mouse.3.5-dpc.bla	gb_est1:AW9821218	38.00	112.46	4.2e+03	848	1	AW9821218	HVSM60002E23f.Hord
gb_est2:BG040075	38.00	116.49	2.5e+03	539	1	BG040075	NXSI_106_B09.F.NXSI.(N	gb_gss:AQ573615	38.00	112.42	4.3e+03	852	1	AQ573615	nbxb0084F19r.CUGI.R
gb_est2:BG0407221	38.00	116.49	2.5e+03	539	1	AQ047221	RPCI11-35P16.TJ.RPCI.(N	gb_hic:AK020369	38.00	112.38	4.3e+03	855	1	AK020369	Mus.musculus.adult
gb_gss:AZ487901	38.00	116.47	2.5e+03	539	1	AZ487901	1M0317B20R.Mouse.10kb	gb_gss:AQ2453714	38.00	112.37	4.3e+03	855	1	AQ2453714	HS_2060.B1.C01.T7.C
gb_gss:AZ4014210	38.00	116.47	2.5e+03	540	1	AZ4014210	RPCI11-20E2.TKBF.RPCI-1	gb_gss:AQ2453714	38.00	112.37	4.3e+03	856	1	AQ2453714	HS_2060.B1.C01.T7.C
gb_est1:AW622560	38.00	116.39	2.6e+03	545	1	AW622560	EST313360.tomato.root	gb_est1:AL346799	38.00	112.35	4.3e+03	858	1	AL346799	AL546799.LTI.NFL006
gb_gss:AZ375161	38.00	116.34	2.6e+03	549	1	AZ375161	1M0128G13f.Mouse.10kb	gb_est2:BG520904	38.00	112.32	4.3e+03	861	1	BG520904	602780803f1.NCI.CGA
gb_gss:AZ3621879	38.00	116.32	2.6e+03	549	1	AZ621879	1M045016f.Mouse.10kb	gb_gss:CN500A08R	38.00	112.30	4.3e+03	863	1	CN500A08R	AL034974.Drosophila.melanoga
gb_est1:BE755889	38.00	116.26	2.7e+03	553	1	BE755889	209768.MARC.2BOV.Bos.t	gb_est1:AL525921	38.00	112.28	4.4e+03	865	1	AL525921	LTI.NFL001
gb_est1:AL040324	38.00	116.16	2.7e+03	563	1	AL040324	DFE2P43C2218.r1.434.C	gb_est1:BE569621	38.00	112.09	4.4e+03	884	1	BE569621	601328268f1.NCI.CGA
gb_est1:AW944238	38.00	116.05	2.7e+03	566	1	AW944238	S002424.3prime.SD.Dros	gb_est2:BI102559	38.00	112.07	4.4e+03	886	1	BI102559	602888119f1.NCI.CGA
gb_est2:BI346612	38.00	116.02	2.7e+03	568	1	BI346612	375864.MARC.2PIC.Sus.s	gb_gss:AQ2453714	38.00	112.37	4.3e+03	856	1	AQ2453714	HS_2060.B1.C01.T7.C
gb_est1:BI195842	38.00	115.97	2.7e+03	571	1	BI195842	70154866.A.A.thaliana,	gb_est1:AL525921	38.00	112.09	4.4e+03	884	1	AL525921	LTI.NFL001
gb_gss:AZ589261	38.00	115.94	2.7e+03	573	1	AV089261	CITBI-EL-2645I19.TF.CI	gb_est2:BE971354	38.00	111.81	4.6e+03	912	1	BE971354	60165152f1.NIH.MGC
gb_est1:AV607797	38.00	115.85	2.7e+03	579	1	AV607797	AV607797.Bos.taurus.ki	gb_gss:CN50610J	38.00	111.68	4.7e+03	925	1	CN50610J	AL399689.T7.end.of.clone.ASO
gb_est1:AA851938	38.00	115.85	2.7e+03	579	1	AA851938	EST194707.Normalized.r	gb_est1:BE270919	38.00	111.64	4.7e+03	930	1	BE270919	600943796f1.NIH.MGC
gb_est2:BG052489	38.00	115.77	2.8e+03	584	1	BG052489	RHI22_13.F11.b1.A003.R	gb_gss:CN501EVK	38.00	111.56	4.7e+03	938	1	CN501EVK	AL141057.Anopheles.gambiae.G
gb_est1:AA034752	38.00	115.74	2.8e+03	586	1	AA034752	ml44b11.r1.Soaress.mou	gb_gss:CN500GGGA	38.00	111.29	4.9e+03	967	1	CN500GGGA	AL397664.T7.end.of.clone.ASO
gb_est1:AI092236	38.00	115.70	2.8e+03	589	1	AI092236	EST237528.Normalized.r	gb_gss:CN503LI14	38.00	111.16	5.0e+03	989	1	CN503LI14	AL249493.Tetraodon.nigrivir
gb_gss:AZ971694	38.00	115.67	2.8e+03	591	1	AZ971694	2M0245J13f.Mouse.10kb	gb_est1:BE745770	38.00	111.09	5.0e+03	989	1	BE745770	601579957f1.NIH.MGC
gb_gss:AZ993364	38.00	115.67	2.8e+03	591	1	AZ993364	2M0278D20f.Mouse.10kb	gb_gss:CN503UBF	38.00	110.98	5.1e+03	1001	1	CN503UBF	AL260916.Tetraodon.nigrivir
gb_est1:AI542097	38.00	115.65	2.8e+03	592	1	AI542097	S008177.3prime.SD.Dros	gb_gss:CN505RL8	38.00	110.77	5.1e+03	1001	1	CN505RL8	AL350693.Tetraodon.nigrivir
gb_est1:AU006094	38.00	115.55	2.8e+03	599	1	AU006094	AU006094.Bombyx.mori.F	gb_est2:BF624742	38.00	110.63	5.3e+03	1041	1	BF624742	HVSM60017J22f.Hor
gb_est2:BE910827	38.00	115.52	2.8e+03	599	1	BE910827	601661889f1.NCI.CGAP.M	gb_est2:BI408103	38.00	110.39	5.5e+03	1070	1	BI408103	602918905f1.NCI.CG
gb_est1:AW011551	38.00	115.52	2.9e+03	601	1	AW011551	S722B07.Pine.TRI.CGAP.M	gb_gss:CN500GGV	38.00	110.35	5.5e+03	1075	1	CN500GGV	AL072600.Drosophila.melanog
gb_gss:AZ974011	38.00	115.52	2.9e+03	601	1	AZ974011	2M0248M02f.Mouse.10kb	gb_gss:AF029645	38.00	110.14	5.7e+03	1101	1	AF029645	AF029645.Salmonell
gb_est1:AW491331	38.00	115.49	2.9e+03	603	1	AW491331	UI-M-BH3-Att-f-04-0-UI	gb_hic:AF348077	38.00	109.37	6.3e+03	1200	1	AF348077	Homo.sapiens.serin
gb_est1:AL041825	38.00	115.47	2.9e+03	604	1	AL041825	DKF2P43C2218.r1.434.C	gb_hic:AF348077	38.00	107.58	7.9e+03	1467	1	AF348077	Homo.sapiens.serin
gb_gss:AZ285038	38.00	115.46	2.9e+03	605	1	AZ285038	602409313f1.NIH.MGC.91	gb_hic:AK004602	38.00	104.56	1.2e+04	2060	1	AK004602	Mus.musculus.adult
gb_est2:BG285038	38.00	115.39	2.9e+03	610	1	BG285038	602409313f1.NIH.MGC.91	gb_hic:AK004602	38.00	102.94	1.4e+04	2474	1	AK004602	Mus.musculus.adult
gb_est1:AL508613	38.00	115.36	2.9e+03	612	1	AL508613	EST2326193.Normalized.r	gb_est1:AA943484	37.50	119.51	1.7e+03	319	1	AA943484	UI-M-AQ1-acc-f-06-0
gb_est2:BI231618	38.00	115.33	2.9e+03	614	1	BI231618	RE22911.3prime.RE.Dros	gb_est1:AA943484	37.50	118.02	2.1e+03	377	1	AA943484	UI-M-AQ1-acc-f-06-0
gb_gss:AZ940787	38.00	115.32	3.0e+03	636	1	AZ940787	S011844.3prime.SD.Dros	gb_est1:BE622610	37.50	116.67	2.5e+03	439	1	BE622610	UI-M-AQ1-acc-f-06-0
gb_est1:AW491331	38.00	115.32	3.0e+03	636	1	AW491331	2M0200J71f.Mouse.10kb	gb_est1:AW458473	37.50	115.58	2.8e+03	496	1	AW458473	sh09f06.y1.Gm-cl016
gb_gss:AZ960833	38.00	115.26	3.0e+03	615	1	AL161580	CITBI-EL-2529B11.TF.CI	gb_est2:BI319134	37.50	116.67	2.5e+03	439	1	BI319134	949039H04.x2.949-
gb_est1:AL161580	38.00	115.26	3.0e+03	615	1	AL161580	A002P78U.Hybrid.aspen	gb_est2:BF023400	37.50	113.73	3.6e+03	608	1	BF023400	ux07f05.y1.Soaress.t
gb_gss:AZ84737	38.00	115.18	3.0e+03	624	1	AQ384737	RPCI11-138L13.TV.RPCI-	gb_est2:BF023400	37.50	113.73	3.6e+03	608	1	BF023400	ux07f05.y1.Soaress.t
gb_gss:AZ843644	38.00	115.14	3.0e+03	627	1	AZ843644	2M0142A08R.Mouse.10kb	gb_est2:BF023400	37.50	113.73	3.6e+03	608	1	BF023400	ux07f05.y1.Soaress.t
gb_est1:AL508613	38.00	115.06	3.0e+03	633	1	AL508613	AL508613.Hordeum.vulga	gb_est2:BF023400	37.50	113.73	3.6e+03	608	1	BF023400	ux07f05.y1.Soaress.t
gb_est2:BG640704	38.00	115.02	3.0e+03	636	1	BG640704	S011844.3prime.SD.Dros	gb_est1:BE622610	37.50	113.05	5.1e+03	826	1	BE622610	601440747f1.NIH.MGC
gb_gss:AZ940787	38.00	114.92	3.1e+03	643	1	AZ940787	2M0200J71f.Mouse.10kb	gb_est1:AW458473	37.50	133.34	290.76	56	1	AW458473	sh09f06.y1.Gm-cl016
gb_gss:AZ960833	38.00	114.86	3.1e+03	649	1	BG691536	2M017H02F.Mouse.10kb	gb_gss:AZ843644	37.00	129.94	449.18	109	1	AZ843644	2M017H02F.Mouse.10k
gb_est2:BG691536	38.00	114.86	3.1e+03	649	1	BG691536	2M017H02F.Mouse.10kb	gb_gss:AZ843644	37.00	129.94	449.18	109	1	AZ843644	2M017H02F.Mouse.10k
gb_gss:AZ0449815	38.00	114.84	3.1e+03	649	1	AQ449815	500004G08.x1.CPTOWAMI3	gb_est2:BF023400	37.00	127.01	654.06	114	1	BF023400	602686461f1.NIH.MGC
gb_est2:BG435345	38.00	114.78	3.1e+03	653	1	BG435345	602507603f1.NIH.MGC.79	gb_gss:AZ624971	37.00	126.12	733.14	126	1	AZ624971	1M0463N20R.Mouse.10
gb_est1:AW943197	38.00	114.66	3.2e+03	662	1	AW943197	LD33749.3prime.ID.Dros	gb_gss:AZ624971	37.00	126.12	733.14	126	1	AZ624971	1M0463N20R.Mouse.10
gb_gss:AZ497544	38.00	114.63	3.2e+03	664	1	AZ497544	1M0324L21f.Mouse.10kb	gb_est2:BF201067	37.00	122.81	1.1e+03	183	1	BF201067	WHE0817-0821.M11.M1
gb_est1:AW5296009	38.00	114.63	3.2e+03	664	1	AW5296009	2M0227G22R.Mouse.10kb	gb_est2:BF201067	37.00	122.81	1.1e+03	183	1	BF201067	WHE0817-0821.M11.M1
gb_gss:AZ503351	38.00	114.55	3.2e+03	670	1	BE377242	601229525f1.NCI.CGAP.M	gb_est2:R29243	37.00	121.88	1.2e+03	203	1	R29243	F1-360D.22.week.old.h
gb_gss:AZ503351	38.00	114.53	3.2e+03	672	1	AZ503351	1M0345D18R.Mouse.10kb	gb_est2:R29243	37.00	121.88	1.2e+03	203	1	R29243	F1-360D.22.week.old.h
gb_gss:AZ0287596	38.00	114.42	3.3e+03	680	1	AZ0287596	nbxb0014N24r.CUGI.Rice	gb_gss:AZ777891	37.00	121.67	1.3e+03	208	1	AZ777891	2M0012A13R.Mouse.10
gb_gss:AZ271547	38.00	114.36	3.3e+03	685	1	AZ271547	RPCI-23-130P18.TV.RPCI	gb_est1:BB415746	37.00	121.67	1.3e+03	208	1	BB415746	BB415746.RIXEN.full
gb_gss:AZ271547	38.00	114.36	3.3e+03	685	1	AK011538	Mus.musculus.10.days.ec	gb_est1:BB415746	37.00	121.67	1.3e+03	208	1	BB415746	BB415746.RIXEN.full
gb_gss:AZ362376	38.00	114.34	3.3e+03	686	1	AG632376	CMA-C70278-221099-027-	gb_gss:AZ25906	37.00	120.58	1.5e+03	235	1	AZ25906	249PB803.Pb.MBN.#21
gb_est2:BG434946	38.00	114.34	3.3e+03	686	1	BG434946	602507207f1.NIH.MGC.79	gb_est1:AA980895	37.00	120.54	1.5e+03	236	1	AA980895	UI-M-CO-hx-a-07-0-U
gb_gss:AZ593787	38.00	114.33	3.3e+03	687	1	AZ593787	1M0405F03R.Mouse.10kb	gb_est1:BB033699	37.00	120.14	1.6e+03	247	1	BB033699	BB033699.RIXEN.full
gb_est1:AW722088	38.00	114.25	3.4e+03	693	1	AW722088	AV722088.HTB.Homo.sapi	gb_est2:D39771	37.00	119.96	1.6e+03	252	1	D39771	RIC51358A.Rice.shoot
gb_est2:BG751479	38.00	114.18	3.4e+03	699	1	BG751479	602735057f1.NIH.MGC.43	gb_est1:BB279406	37.00	119.79	1.7e+03	257	1	BB279406	BB279406.RIXEN.full
gb_est2:BG086072	38.00	114.16	3.4e+03	700	1	BG086072	H3121D12-5.N1A.Mouse.1	gb_gss:AZ25906	37.00	119.79	1.7e+03	257	1	AZ25906	

gb_est2:BF925624	37.00	118.80	1.9e+03	287	BF925624	CM2-NT0192-291100-578-	gb_est2:D26782	37.00	115.40	2.9e+03	421	D26782	CELK002DGR	Yuji Kohar	
gb_gss:AB328570	37.00	118.80	1.9e+03	287	AB328570	IM0052H24F	Mouse 10kb	gb_est1:AA147516	37.00	115.33	2.9e+03	424	AA147516	zhe150f02.r1	Soares_p
gb_est1:BB339475	37.00	118.77	1.9e+03	288	B339475	BB339475	R1KEN full-le	gb_est1:BA446737	37.00	115.33	2.9e+03	424	BA446737	WHE1140_H11	P222S_W
gb_est1:BB756031	37.00	118.74	1.9e+03	289	BB756031	sl112g11.v1	Gm-cl036	gb_est2:BF471720	37.00	115.27	2.9e+03	427	BF471720	UI-M-BH3-avw-c-08-0	
gb_est1:BB295953	37.00	118.65	1.9e+03	292	B295953	BB295953	R1KEN full-le	gb_est2:BF651413	37.00	115.27	2.9e+03	427	BF651413	274196	MARC 3BOV
gb_gss:AB284807	37.00	118.65	1.9e+03	292	AB284807	RPCI-23-19IK12	TV RPCI	gb_est2:BF523343	37.00	115.25	3.0e+03	428	BF523343	M35H10STM	Arabidops
gb_est2:BF932996	37.00	118.62	1.9e+03	293	BF932996	ye29a03.s1	Stratagene	gb_est2:BF62237	37.00	115.21	3.0e+03	428	BF62237	yb97H17.s1	Stratagene
gb_est2:BF387101	37.00	118.56	1.9e+03	295	BF387101	UI-R-CAL-bbkd-d-04-0-UI		gb_est1:BE186864	37.00	115.21	3.0e+03	430	BE186864	946013F10.X1	946 -
gb_est1:AA467249	37.00	118.47	2.0e+03	298	AA467249	VF06a07.r1	Knowles	gb_gss:AB2837155	37.00	115.21	3.0e+03	430	AB2837155	2M01321F	Mouse 10
gb_est1:AA204556	37.00	118.44	2.0e+03	298	AA204556	AV204556	R1KEN full-le	gb_gss:AB2837155	37.00	115.21	3.0e+03	430	AB2837155	2M01321F	Mouse 10
gb_est2:BG014250	37.00	118.41	2.0e+03	300	BG014250	CM3-GN0296-211200-574-		gb_est1:BE481504	37.00	115.19	3.0e+03	431	BE481504	166578	BARC 5BOV
gb_est2:BG315743	37.00	118.29	2.0e+03	304	BG315743	sab84040.y1	Gm-cl032	gb_est1:BE481504	37.00	115.15	3.0e+03	433	BE481504	166578	BARC 5BOV
gb_est1:BB259431	37.00	118.23	2.0e+03	306	B259431	BB259431	R1KEN full-le	gb_gss:AB283647	37.00	115.13	3.0e+03	434	AB283647	RPCI-23-125F23	TV R
gb_est1:BB541515	37.00	118.21	2.0e+03	307	BB541515	BB541515	R1KEN full-le	gb_gss:AB283608	37.00	115.09	3.0e+03	436	AB283608	CELK033CAR	Yuji Kohar
gb_gss:AA48080P	37.00	118.21	2.0e+03	307	AA48080P	T. brucei	sheared	gb_est2:D34120	37.00	115.09	3.0e+03	436	D34120	CELK041CAR	Yuji Kohar
gb_est1:BB3611183	37.00	118.12	2.0e+03	310	BB3611183	BB2411183	R1KEN full-le	gb_est2:BF8748	37.00	115.09	3.0e+03	436	BF8748	Y189h02.s1	Soares Inf
gb_est1:BB3611156	37.00	118.12	2.0e+03	310	BB3611156	BB3611156	R1KEN full-le	gb_est2:BF8748	37.00	115.09	3.0e+03	436	BF8748	Y189h02.s1	Soares Inf
gb_gss:AA2050958	37.00	118.03	2.1e+03	313	AA2050958	GSSRC11809	Trypanosoma	gb_est2:BF69901	37.00	115.07	3.0e+03	437	BF69901	UI-M-BH3-atw-h-12-0	
gb_est1:AB381755	37.00	117.78	2.1e+03	322	AB381755	te40g05.x1	Soares_NHMK	gb_est2:BF808552	37.00	115.07	3.0e+03	437	BF808552	CM1-CI0092-141100-5	
gb_est2:BF12630	37.00	117.75	2.1e+03	323	BF12630	MR3-UT0050-211100-002-		gb_est2:BF606706	37.00	115.05	3.0e+03	438	BF606706	273820	MARC 3BOV
gb_est2:BF912629	37.00	117.73	2.2e+03	324	BF912629	MR3-UT0050-211100-002-		gb_est2:D26780	37.00	115.03	3.0e+03	439	D26780	CELK011GZR	Yuji Kohar
gb_est2:BF1060450	37.00	117.70	2.2e+03	325	BF1060450	MR3-UT0050-220101-001-		gb_est1:AA493914	37.00	115.01	3.1e+03	440	AA493914	nh07d09.s1	NCI_CGAP
gb_gss:AB2886942	37.00	117.59	2.2e+03	329	AB2886942	RPCI-23-195G16	TJ RPCI	gb_gss:AB2886942	37.00	115.01	3.1e+03	440	AB2886942	UI-M-BH3-avw-c-07-0	
gb_est2:F00349	37.00	117.43	2.2e+03	335	F00349	HSB10G062	STRATAGENE	gb_est1:AW312777	37.00	114.99	3.1e+03	441	AW312777	5072	MARC 2BOV
gb_est2:BF06705	37.00	117.43	2.2e+03	335	BF06705	273819	MARC 3BOV	gb_est1:AW312777	37.00	114.99	3.1e+03	441	AW312777	5072	MARC 2BOV
gb_est2:BF771932	37.00	117.30	2.3e+03	340	BF771932	IL5-IT0029-291100-259-		gb_gss:AB28288	37.00	114.94	3.1e+03	443	AB28288	T9D20H8	TAMU Arabidop
gb_est1:AW084922	37.00	117.25	2.3e+03	342	AW084922	xc65f02.x1	NCI_CGAP	gb_est1:AA027867	37.00	114.88	3.1e+03	446	AA027867	zk05b03.r1	Soares_p
gb_est1:BE525030	37.00	117.22	2.3e+03	343	BE525030	M57G15PM	Arabidopsis	gb_gss:AA027867	37.00	114.85	3.1e+03	448	AA027867	zk05b03.r1	Soares_p
gb_est2:T00280	37.00	117.22	2.3e+03	343	T00280	eST01001	Early embryo	gb_gss:AA027867	37.00	114.85	3.1e+03	448	AA027867	zk05b03.r1	Soares_p
gb_est1:AW312775	37.00	117.19	2.3e+03	344	AW312775	5089	MARC 2BOV	gb_gss:AA027867	37.00	114.85	3.1e+03	448	AA027867	zk05b03.r1	Soares_p
gb_est2:D34104	37.00	117.14	2.3e+03	346	D34104	CELK041A6R	Yuji Kohara	gb_est2:BF044495	37.00	114.83	3.1e+03	449	BF044495	BP25003A010F11	Soar
gb_est2:BF425560	37.00	117.12	2.3e+03	347	BF425560	CS91859	Rice panicle	gb_est2:BF957382	37.00	114.83	3.1e+03	449	BF957382	RC4-3060231-241100-3	
gb_est2:BF109290	37.00	117.07	2.4e+03	349	BF109290	7u54h04.y1	Gm-cl068	gb_gss:AA024202	37.00	114.83	3.1e+03	449	AA024202	HS-3060242	MR C
gb_est2:BG5111006	37.00	116.94	2.4e+03	354	BG5111006	7u54h04.y1	Gm-cl068	gb_est1:AA024202	37.00	114.83	3.1e+03	449	AA024202	HS-3060242	MR C
gb_est1:AW296961	37.00	116.86	2.4e+03	357	AW296961	UI-H-BW0-ajfc-r1	0-0-UI	gb_gss:AA024202	37.00	114.81	3.1e+03	450	AA024202	DGL-5_H06_g1	AA002
gb_est1:AW210468	37.00	116.77	2.4e+03	361	AW210468	um59e02.x1	Sugano	gb_gss:AA024202	37.00	114.79	3.1e+03	451	AA024202	DGL-5_H06_g1	AA002
gb_est2:D32780	37.00	116.72	2.5e+03	363	D32780	CELK0219B3R	Yuji Kohara	gb_est1:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_gss:AB27459	37.00	116.69	2.5e+03	366	AB27459	T8L10TR	TAMU Arabidopsis	gb_est1:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW491167	37.00	116.62	2.5e+03	367	AW491167	UI-M-BH3-atn-d-07-0-UI		gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est2:R31381	37.00	116.62	2.5e+03	367	R31381	YH75605.r1	Soares	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW161087	37.00	116.52	2.5e+03	371	AW161087	vr54h04.y1	Knowles	gb_est1:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_gss:AB2849226	37.00	116.47	2.5e+03	373	AB2849226	2M0150N01R	Mouse 10kb	gb_est1:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.29	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202	ST05H05	Pine Triple
gb_est1:AW036015	37.00	116.22	2.6e+03	381	AW036015	EST283099	tomato	gb_gss:AA024202	37.00	114.75	3.2e+03	453	AA024202</		

```

gb_est2:BF558068 - 37.00 114.05 3.5e+03 490 1 BF558068 UI-R-CO-hj-g-09-0-UI.1
gb_est1:AF083303 + 37.00 114.03 3.5e+03 491 1 AF083303 AF083303 Drosophila me
gb_est1:AI494302 - 37.00 114.03 3.5e+03 491 1 AI494302 QY98e10.xl NCI_CGAP_BI
gb_gss:BH085545 - 37.00 114.03 3.5e+03 491 1 BH085545 RPTI-24-310A2.TV RPTI-
gb_gss:AQ674982 + 37.00 114.01 3.5e+03 492 1 AQ674982 HS_2161.AL_H01.T7C CIT
gb_est1:AW586740 + 37.00 113.98 3.5e+03 494 1 AW586740 EST318363 MHAM Medicag
gb_est2:BF497115 + 37.00 113.98 3.5e+03 494 1 BF497115 AT11189.5Prime AT Dros
gb_gss:AZ344778 + 37.00 113.98 3.5e+03 494 1 AZ344778 IM0079E02F Mouse 10kb
gb_gss:AQ037915 + 37.00 113.96 3.5e+03 495 1 AQ037915 CIT-HSP-232SG5.TV CIT-
gb_est1:AA394318 + 37.00 113.94 3.5e+03 496 1 AA394318 25915 Lambda-PRL2 Arab

seq_name: gb_est1:BE659955

seq_documentation_block:
LOCUS BE659955 711 bp mRNA EST 06-SEP-2000
DEFINITION 1077 GmaxSC Glycine max cDNA, mRNA sequence.
ACCESSION BE659955
VERSION BE659955.1 GI:9985949
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE 1 (bases 1 to 711)
AUTHORS Harris, N., Chapman, B.P. and Gijzen, M.
TITLE Gene expression in developing soybean seed coats
JOURNAL Unpublished (2000)
COMMENT Contact: Gijzen M
Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: gijzenm@agr.ca.
FEATURES
source
1..711
Location/Qualifiers
/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
/tissue_type="Seed coats"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from green seed coats in mid to late developmental stage
, average fresh weight 250 mg per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adapters and the products were digested
with blunt-ended cDNA fragments and the products were ligated
with XhoI for directional cloning into Lambda ZAP Express
vector. This lambda library was amplified once using E.
coli host strain XL1 Blue MRF'. Inserts were then
subcloned by mass excision using ExAssist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XL0LR."

BASE COUNT 186 a 207 c 179 g 134 t 5 others
ORIGIN
alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-485-529-104 x BE659955
Align seg 1/1 to: BE659955 from: 1 to: 711
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||

gb_est2:BF558068 - 37.00 114.05 3.5e+03 490 1 BF558068 UI-R-CO-hj-g-09-0-UI.1
gb_est1:AF083303 + 37.00 114.03 3.5e+03 491 1 AF083303 AF083303 Drosophila me
gb_est1:AI494302 - 37.00 114.03 3.5e+03 491 1 AI494302 QY98e10.xl NCI_CGAP_BI
gb_gss:BH085545 - 37.00 114.03 3.5e+03 491 1 BH085545 RPTI-24-310A2.TV RPTI-
gb_gss:AQ674982 + 37.00 114.01 3.5e+03 492 1 AQ674982 HS_2161.AL_H01.T7C CIT
gb_est1:AW586740 + 37.00 113.98 3.5e+03 494 1 AW586740 EST318363 MHAM Medicag
gb_est2:BF497115 + 37.00 113.98 3.5e+03 494 1 BF497115 AT11189.5Prime AT Dros
gb_gss:AZ344778 + 37.00 113.98 3.5e+03 494 1 AZ344778 IM0079E02F Mouse 10kb
gb_gss:AQ037915 + 37.00 113.96 3.5e+03 495 1 AQ037915 CIT-HSP-232SG5.TV CIT-
gb_est1:AA394318 + 37.00 113.94 3.5e+03 496 1 AA394318 25915 Lambda-PRL2 Arab

seq_name: gb_est2:BF268018

seq_documentation_block:
LOCUS BF268018 844 bp mRNA EST 09-MAR-2001
DEFINITION HV_CEA0019J17f Hordeum vulgare seedling green leaf EST library
HV_CEA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEA0019J17f, mRNA sequence.
ACCESSION BF268018
VERSION BF268018.2 GI:13263734
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 844)
AUTHORS Wing, R., Close, R.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
TITLE Development of a genetically and physically anchored EST resource
for barley genomics
JOURNAL Unpublished (2000)
COMMENT On Nov 17, 2000 this sequence version replaced gi:11199013.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCGCTCACTAAAGGG
High quality sequence stop: 587.
FEATURES
source
1..844
Location/Qualifiers
/organism="Hordeum vulgare"
/cultivar="C116155 (M1a13)"
/db_xref="taxon:4513"
/clone_lib="HV_CEA0019J17f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; For
more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"

BASE COUNT 150 a 290 c 276 g 128 t
ORIGIN
alignment_scores:
Quality: 81.00 Length: 17
Ratio: 4.765 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-485-529-104 x BF268018
Align seg 1/1 to: BF268018 from: 1 to: 844
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
260 GAGCAGCTGCTGGCGGCTCGGCTACAGGTGGCGGCTCCGACATGGC 309
17 a 17

```

```
310 G 310
seq_name: gb_est2:D39460

seq_documentation_block: 263 bp mRNA EST 11-NOV-1994
LOCUS D39460 RICE SHOOT Oryza sativa cDNA, mRNA sequence.
DEFINITION RICS0803A Rice shoot Oryza sativa cDNA, mRNA sequence.
ACCESSION D39460
VERSION D39460.1 GI:568611
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 263)
AUTHORS Sasaki,T., Miyao,A. and Yamamoto,K.
TITLE Rice cDNA from callus 1995
COMMENT Unpublished (1995)
CONTACT: Takuji Sasaki
NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES
RICE GENOME RESEARCH PROGRAM, KANNONDAI 2-1-2, TSUKUBA, IBARAKI
305-8602, JAPAN
TEL: 81-298-38-7441
FAX: 81-298-38-7468
EMAIL: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/.

FEATURES
    source
        1..263
            /organism="Oryza sativa"
            /strain="Nipponbare, sub_species Japonica"
            /db_xref="taxon:4530"
            /clone_lib="Rice shoot"
            /note="Etiolated shoot (8 days old)"
BASE COUNT 46 a 64 c 116 g 35 t 2 others
ORIGIN
|||||
1 AspGluLeuAlaLaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
97 GACGAGCTGTCGGCGCGCTGCGGTACAAAGTGGCTCGCATGGC 146
|||||
17 a 17
147 C 147

seq_name: gb_est1:AV410222

seq_documentation_block: 355 bp mRNA EST 23-MAY-2000
LOCUS AV410222 Lotus japonicus young plants (two-week old) Lotus
DEFINITION AV410222 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWL069f02_r 5', mRNA sequence.
ACCESSION AV410222
VERSION AV410222.1 GI:7723076
KEYWORDS EST.
SOURCE Lotus japonicus.
ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.
REFERENCE 1 (bases 1 to 355)
AUTHORS Asanizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE Generation of 7137 non-redundant expressed sequence tags from a

legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
    source
        1..355
            /organism="Lotus japonicus"
            /db_xref="taxon:34305"
            /clone="MWL069f02_r"
            /clone_lib="Lotus japonicus young plants (two-week old)"
            /dev_stage="Lotus japonicus (two-week old)"
            /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
            XhoI; isolate=Miyakojima MG-20"
BASE COUNT 94 a 70 c 101 g 90 t
ORIGIN
|||||
1 AspGluLeuAlaLaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
241 GATGAGCTTCTGGCGGCTTAGGTACAAAGTGGCTTCCTCTGACATGGC 290
|||||
17 a 17
291 T 291

seq_name: gb_est1:BE321891

seq_documentation_block: 372 bp mRNA EST 21-DEC-2000
LOCUS BE321891 Insect herbivory Medicago truncatula cDNA clone
DEFINITION NF045B07IN1F1058 Insect herbivory Medicago truncatula cDNA clone
NF045B07IN 5', mRNA sequence.
ACCESSION BE321891
VERSION BE321891.2 GI:11964088
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 372)
AUTHORS Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula insect herbivory library
JOURNAL Unpublished (2000)
COMMENT On Jul 14, 2000 this sequence version replaced gi:9195668.
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7601
Email: kkorthe@comp.uark.edu
Medicago Genome Initiative accession: MGI:S:23522
Insert length: 798 Std Error: 0.00
Plate: 045 row: B column: 07
Seq primer: TCACACGAGGAACAGCATGAC.
Location/Qualifiers
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source
1. .372
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF045B07IN"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
BASE COUNT      153 a      66 c      72 g      81 t
ORIGIN

alignment_scores:
Quality: 78.00      Length: 17
Ratio: 4.588      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x BE321891 ..

Align seg 1/1 to: BE321891 from: 1 to: 372

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
247 GACGAGTCTTACGACCATAGTTACAGGTTCGCTCTTCGACATGCG 296
17 a 17
297 T 297

seq_name: gb_est2:C27475

seq_documentation_block:
LOCUS C27475 388 bp mRNA EST 06-AUG-1997
DEFINITION C27475 Rice callus cDNA Oryza sativa cDNA clone C51976_1A, mRNA
sequence.
ACCESSION C27475
VERSION C27475.1 GI:2311320
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 388)
AUTHORS Yamamoto,K. and Sasaki,T.
TITLE Rice cDNA from callus 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@r.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES
Location/Qualifiers
1. .388
/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="C51976_1A"
/tissue_type="callus cDNA"
/dev_stage="callus"

BASE COUNT      83 a      102 c      134 g      65 t      4 others
ORIGIN

alignment_scores:

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Quality: 78.00      Length: 17
Ratio: 4.588      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x C27475 ..

Align seg 1/1 to: C27475 from: 1 to: 388

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
271 GACGAGCTCTCGCGCGCTCGGTACAGGTCCGCTCTTCGACATGCG 320
17 a 17
321 C 321

seq_name: gb_est1:AL369357

seq_documentation_block:
LOCUS AL369357 399 bp mRNA EST 03-AUG-2000
DEFINITION MtBA30E09F1 MtBA Medicago truncatula cDNA clone MtBA30E09 T3, mRNA
sequence.
ACCESSION AL369357
VERSION AL369357.1 GI:9669110
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolaeae;
Medicago.
REFERENCE 1 (bases 1 to 399)
AUTHORS Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson,
V. and Gamas,P.
TITLE Medicago truncatula ESTs from nitrogen-starved roots
JOURNAL Unpublished (2000)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).

FEATURES
Location/Qualifiers
1. .399
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA30E09"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="vector: pBluescript PSK; Site.1: EcoRI; Site.2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
BASE COUNT      166 a      74 c      75 g      84 t
ORIGIN

alignment_scores:

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Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AL369357 ..

Align seg 1/1 to: AL369357 from: 1 to: 399

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
285 GACGAGTGTAGCAGCATAGGTACAAAGGTCGCTTCGACATGGC 334

17 a 17

335 T 335

seq_name: gb_est1:AU091413

seq_documentation_block: 399 bp mRNA EST 05-JUN-2000
LOCUS AU091413 Rice cDNA from immature leaf including apical meristem
DEFINITION AU091413 (under short day condition) Oryza sativa cDNA clone E60220, mRNA
sequence.
ACCESSION AU091413
VERSION AU091413.1 GI:8251089
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 399)
Sasaki,T. and Yamamoto,K.
Rice cDNA from immature leaf including apical meristem (2000)
AUTHORS Unpublished (2000)
TITLE National Institute of Agrobiological Resources
JOURNAL Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
COMMENT 305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT "RGP".
E60220_1A.

FEATURES

Source

Location/Qualifiers
1..399

/organism="Oryza sativa"
/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E60220"
/clone_lib="Rice cDNA from immature leaf including apical
meristem (under short day condition)"
/dev_stage="immature leaf including apical meristem (under
short day condition)"

BASE COUNT 81 a 122 c 117 g 79 t
ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AU091413 ..

Align seg 1/1 to: AU091413 from: 1 to: 399

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
346 GACGAGTGTCTCGGCGCTCGGGTACAAAGTGGTGGTCCGACATGGC 395

17 a 17

396 C 396

seq_name: gb_est1:AL369482

seq_documentation_block: 458 bp mRNA EST 03-AUG-2000
LOCUS AL369482 MtBA31D06F1 MtBA Medicago truncatula cDNA clone MTBA31D06 T3, mRNA
DEFINITION AL369482
sequence.
ACCESSION AL369482
VERSION AL369482.1 GI:9669235
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 458)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
V. and Gamas,P.
Medicago truncatula ESTs from nitrogen-starved roots
Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

CONTACT : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).

Location/Qualifiers
1..458

/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA31D06"
/clone_lib="MtBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript PSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using GigaPack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exassit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."

FEATURES

Source

Location/Qualifiers
1..458

/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA31D06"
/clone_lib="MtBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript PSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using GigaPack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exassit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."

BASE COUNT 172 a 97 c 82 g 107 t
ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AL369482 ..

Align seg 1/1 to: AL369482 from: 1 to: 458

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
273 GACGAGTGTGTAGCAGCATAGGTACAAAGGTTTCGCTTCGACATGGC 322

17 a 17
|
323 T 323

seq_name: gb_est1:AL371425

seq_documentation_block: 466 bp mRNA EST 03-AUG-2000
LOCUS AL371425
DEFINITION MTBA44B05F1 MTBA Medicago truncatula cDNA clone MTBA44B05 T3, mRNA
sequence.

ACCESSION AL371425

VERSION AL371425.1 GI:9671178

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 466)

AUTHORS
Journet,E.P., Crespeau,H., van-Tuinen,D., Gouzy,J., Jaillon,O.,
Niebel,A., Carreau,V., Chatagnier,O., Kahn,D., Gianinazzi-Pearson
,V. and Gamas,P.

TITLE Medicago truncatula ESTs from nitrogen-starved roots

JOURNAL Unpublished (2000)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-est@toulouse.inra.fr Website :
http://sequence.toulouse.inra.fr/Mtruncatula.html).

FEATURES

source

1. .466
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA44B05"
/clone_lib="MtBA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/note="vector: pluescript psk; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using Exsist helper phage
and propagated in souk cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
BASE COUNT 183 a 93 c 82 g 108 t
ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AL371425 ..

Align seg 1/1 to: AL371425 from: 1 to: 466

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||

283 GACGAGTGTGTAGCAGCATAGTACAAAGGTTCGCTCTCCGACATGCC 332

17 a 17
|
333 T 333

seq_name: gb_est1:AU222715

seq_documentation_block: 467 bp mRNA EST 30-JUL-2001
LOCUS AU222715
DEFINITION AU222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence.
ACCESSION AU222715
VERSION AU222715.1 GI:15008327

KEYWORDS EST.

SOURCE Oryza sativa.

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 467)

AUTHORS Sasaki,T. and Yamamoto,K.

TITLE Rice cDNA from etiolated shoot (2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan

Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/

PROJECT "RGP"

S0583_97A.

Location/Qualifiers

1. .467

/organism="Oryza sativa"

/strain="Nipponbare, sub_species Japonica"

/db_xref="taxon:4530"

/clone="S0583"

/clone_lib="Rice shoot"

/note="Etiolated shoot (8 days old)"

BASE COUNT 90 a 136 c 176 g 65 t

ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AU222715 ..

Align seg 1/1 to: AU222715 from: 1 to: 467

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||

198 GACGAGTGTGTAGCAGCATAGTACAAAGGTTCGCTCTCCGACATGCC 247

17 a 17
|
248 C 248

seq_name: gb_est1:AV422153

seq_documentation_block:

LOCUS AV422153 484 bp mRNA EST 23-MAY-2000
DEFINITION AV422153 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWM005b04_r 5', mRNA sequence.

ACCESSION AV422153

VERSION AV422153.1 GI:7776718

KEYWORDS EST.

SOURCE Lotus japonicus.

ORGANISM

Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.

REFERENCE 1 (bases 1 to 484)
 AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
 TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
 JOURNAL DNA Res. 7 (2), 127-130 (2000)
 MEDLINE 20277479
 COMMENT Contact: Yasukazu Nakamura
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
 source
 1..484
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone="MWM005b04_r"
 /clone_lib="Lotus japonicus young plants (two-week old)"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate=Miyakojima MG-20".

BASE COUNT 130 a 144 c 103 g 107 t
 ORIGIN

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
 US-09-485-529-104 x AV422153 ..

Align seg 1/1 to: AV422153 from: 1 to: 484

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 ||||||||||||||||||||||||||||||||||||||||||||
 81 GATGAGGTTCTGCGGGTTAGGTACAAAGTTCCTCGCATGGC 130

17 a 17
 |
 131 T 131

seq_name: gb_estl:AW697326

seq_documentation_block:
 LOCUS AW697326 537 bp mRNA EST 20-DEC-2000
 DEFINITION NF117E10ST1F1082 Developing stem Medicago truncatula cDNA clone
 ACCESSION AW697326
 VERSION AW697326.2 GI:11933520
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 537)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
 ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
 ,R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7572088.
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380

Email: radixon@noble.org
 Insert Length: 686 Std Error: 0.00
 Plate: 117 row: E column: 10
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
 source
 1..537
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF117E10ST"
 /clone_lib="Developing stem"
 /tissue_type="stem"
 /dev_stage="pooled developmental"
 /note="Vector: Lambda zap; Contains a mixture of
 internodal stem segments".

BASE COUNT 199 a 120 c 87 g 131 t
 ORIGIN

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
 US-09-485-529-104 x AW697326 ..

Align seg 1/1 to: AW697326 from: 1 to: 537

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 ||||||||||||||||||||||||||||||||||||||||||||
 337 GACGAGTTGTTAGCAGCATTAGGTACAAAGTTCGCTCCGACATGGC 386

17 a 17
 |
 387 T 387

seq_name: gb_estl:AW695914

seq_documentation_block:
 LOCUS AW695914 559 bp mRNA EST 21-DEC-2000
 DEFINITION NF099H09ST1F1079 Developing stem Medicago truncatula cDNA clone
 ACCESSION AW695914
 VERSION AW695914.2 GI:11957271
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 559)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
 ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
 ,R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7570676.
 Contact: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380

Email: radixon@noble.org
 Insert Length: 654 Std Error: 0.00
 Plate: 099 row: H column: 09
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
 source
 1..559
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"

```

/clone="NF099H05ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/notes="Vector: Lambda zap; Contains a mixture of
intermodal stem segments"
BASE COUNT      197 a      121 c      83 g      158 t
ORIGIN

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alignment_scores:
  Quality:      78.00      Length:      17
  Ratio:        4.588      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 94.118

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```
alignment_block:
US-09-485-529-104 x AW695914 ..
```

```
Align seg 1/1 to: AW695914 from: 1 to: 559
```

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1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
414 GACGAGTTGTTAGCAGCATAGTTACAAGGTTGCTCTTCGACATGGC 463

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17 a 17
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464 T 464
```

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seq_name: gb_est2:BI308816
```

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seq_documentation_block:
LOCUS      BI308816      614 bp      mRNA      EST      20-JUL-2001
DEFINITION EST530226 GP0D Medicago truncatula cDNA clone pGP0D-8H2 5' end,
mRNA sequence.
ACCESSION  BI308816
VERSION     BI308816.1 GI:14983143
KEYWORDS   EST.
SOURCE      Medicago truncatula
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 614)
Grusak, M.A., Sanac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho
J., and Fraser, C.M.
ESTs from developing reproductive tissues of Medicago truncatula
Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B395671e
TIGR sequence name: WFOAX37TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gTg gAT CC).
Location/Qualifiers
1..614
/organism="Medicago truncatula"
/cultivar="Al7"
/db_xref="taxon:3880"
/clone="pgPOD-8H2"
/clone_lib="GP0D"
/dev_stage="Immature pods, ranging in age from 15 to 30
days after pollination"
/notes="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Immature pods, ranging in age from 15 to 30 days
after pollination, were collected from greenhouse-grown
plants. At harvest, seeds were removed from pods and

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FEATURES
source
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isolated pod walls were collected and immediately frozen
in liquid nitrogen. Pod walls were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III
Gold packaging extracts. Plasmids containing cDNA inserts
were excised from the recombinant lambda-zap phage using
Ex-assist helper phage and propagated in XL0LR cells."
BASE COUNT      220 a      130 c      114 g      150 t
ORIGIN

```

```

alignment_scores:
  Quality:      78.00      Length:      17
  Ratio:        4.588      Gaps:        0
Percent Similarity: 100.000 Percent Identity: 94.118

```

```
alignment_block:
US-09-485-529-104 x BI308816 ..
```

```
Align seg 1/1 to: BI308816 from: 1 to: 614
```

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1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
236 GACGAGTTGTTAGCAGCATAGTTACAAGGTTGCTCTTCGACATGGC 285

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17 a 17
```

```
286 T 286
```

```
seq_name: gb_est1:AW694061
```

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seq_documentation_block:
LOCUS      AW694061      655 bp      mRNA      EST      15-JUN-2000
DEFINITION NF072A05ST1F1036 Developing stem Medicago truncatula cDNA clone
NF072A05ST 5', mRNA sequence.
ACCESSION  AW694061
VERSION     AW694061.1 GI:7568798
KEYWORDS   EST.
SOURCE      barrel medic.
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 655)
He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Dixon
R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 655 Std Error: 0.00
Plate: 072 row: A column: 05
Seq primer: TCACACAGGAACACAGCATGAC.
Location/Qualifiers
1..655
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF072A05ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/notes="vector: Lambda zap; Contains a mixture of
intermodal stem segments"
242 a      144 c      109 g      160 t

```

```

TITLE
JOURNAL
COMMENT

```

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FEATURES
source
```

ORIGIN

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AW694061 ..

Align seg 1/1 to: AW694061 from: 1 to: 655

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 298 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTCGCTCCGACATGGC 347

17 a 17

348 T 348

seq_name: gb_est1:AW694064

seq_documentation_block: 656 bp mRNA EST 15-JUN-2000
 LOCUS AW694064
 DEFINITION NF072A07ST1052 Developing stem Medicago truncatula cDNA clone

ACCESSION AW694064

VERSION NF072A07ST 5', mRNA sequence.

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 656)

AUTHORS He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
 , C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
 , R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula stem library

COMMENT Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 656 Std Error: 0.00

Plate: 072 row: A column: 07

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

Location/Qualifiers

1..656

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF072A07St"

/clone_lib="Developing stem"

/tissue_type="stem"

/dev_stage="pooled developmental"

/note="Vector: Lambda Zap; Contains a mixture of

internodal stem segments"

238 a 145 c 107 g 166 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AW694064 ..

Align seg 1/1 to: AW694064 from: 1 to: 656

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 305 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTCGCTCCGACATGGC 354

17 a 17

355 T 355

seq_name: gb_est1:AW696350

seq_documentation_block:

LOCUS AW696350 667 bp mRNA EST 15-JUN-2000
 DEFINITION NF107A12ST1F1088 Developing stem Medicago truncatula cDNA clone

NF107A12ST 5', mRNA sequence.

ACCESSION AW696350

VERSION AW696350.1 GI:7571200

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 667)

AUTHORS He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
 , C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
 , R.A.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula stem library

COMMENT Unpublished (2000)

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 667 Std Error: 0.00

Plate: 107 row: A column: 12

Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES

Location/Qualifiers

1..667

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF107A12St"

/clone_lib="Developing stem"

/tissue_type="stem"

/dev_stage="pooled developmental"

/note="Vector: Lambda Zap; Contains a mixture of

internodal stem segments"

234 a 147 c 126 g 160 t

BASE COUNT

ORIGIN

alignment_scores:

Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:

US-09-485-529-104 x AW696350 ..

Align seg 1/1 to: AW696350 from: 1 to: 667

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 254 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTCGCTCCGACATGGC 303

17 a 17

304 T 304

seq_name: gb_est1:AW584593

seq_documentation_block:
 LOCUS AW584593 683 bp mRNA EST 07-SEP-2000
 DEFINITION N210669e MHAM Medicago truncatula/Glomus versiforme mixed EST
 library cDNA clone MHAM-2p17, mRNA sequence.
 ACCESSION AW584593
 VERSION AW584593.1 GI:7261647
 KEYWORDS EST.
 SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
 ORGANISM Medicago truncatula/Glomus versiforme mixed EST library
 Eukaryote; mixed EST libraries.
 REFERENCE 1 (bases 1 to 683)
 AUTHORS Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
 Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
 ESTs from roots of Medicago truncatula after colonization with
 Glomus versiforme
 JOURNAL Unpublished (2000)
 COMMENT Contact: Harrison M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Other name: MHAM-2c-H09; Date: 3/14/00; Updated to the Database of
 Expressed Sequence Tags (dbEST) on 04/27/00; More information is
 available at 'http://chryslie.tamu.edu/medicago'.
 Seq primer: T3.

FEATURES
 Location/Qualifiers
 source 1..683
 /organism="Medicago truncatula/Glomus versiforme mixed EST
 library"
 /cultivar="Medicago truncatula genotype A17"
 /db_xref="taxon:119092"
 /clone="MHAM-2p17"
 /clone_lib="MHAM"
 /tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
 post-inoculation with Glomus versiforme. The library was
 made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 roots harvested at 10, 17, 22, 31 and 38 days
 post-inoculation with Glomus versiforme. The cDNA was
 directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-assist
 helper phage and propagated in XL0LR cells."
 BASE COUNT 244 a 152 c 114 g 173 t
 ORIGIN

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
 US-09-485-529-104 x AW584593 ..

Align seg 1/1 to: AW584593 from: 1 to: 683

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 |||
 317 GACGAGTGTTCACGACATAGTTACAGGTCGCTCTCCGACATGCC 366

17 a 17

367 T 367

seq_name: gb_est1:AW584661

seq_documentation_block:
 LOCUS AW584661 701 bp mRNA EST 07-SEP-2000
 DEFINITION N210765e MHAM Medicago truncatula/Glomus versiforme mixed EST
 library cDNA clone MHAM-2p18, mRNA sequence.
 ACCESSION AW584661
 VERSION AW584661.1 GI:7261715
 KEYWORDS EST.
 SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
 ORGANISM Medicago truncatula/Glomus versiforme mixed EST library
 Eukaryote; mixed EST libraries.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
 Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
 ESTs from roots of Medicago truncatula after colonization with
 Glomus versiforme
 JOURNAL Unpublished (2000)
 COMMENT Contact: Harrison M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Other name: MHAM-2d-H09; Date: 3/14/00; Updated to the Database of
 Expressed Sequence Tags (dbEST) on 04/27/00; More information is
 available at 'http://chryslie.tamu.edu/medicago'.
 Seq primer: T3.

FEATURES
 Location/Qualifiers
 source 1..701
 /organism="Medicago truncatula/Glomus versiforme mixed EST
 library"
 /cultivar="Medicago truncatula genotype A17"
 /db_xref="taxon:119092"
 /clone="MHAM-2p18"
 /clone_lib="MHAM"
 /tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
 post-inoculation with Glomus versiforme. The library was
 made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 roots harvested at 10, 17, 22, 31 and 38 days
 post-inoculation with Glomus versiforme. The cDNA was
 directionally ligated into the Unizap XR vector from
 Stratagene and packaged using Gigapack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-Zap phage using Ex-assist
 helper phage and propagated in XL0LR cells."
 BASE COUNT 250 a 158 c 118 g 175 t
 ORIGIN

alignment_scores:
 Quality: 78.00 Length: 17
 Ratio: 4.588 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 94.118

alignment_block:
 US-09-485-529-104 x AW584661 ..

Align seg 1/1 to: AW584661 from: 1 to: 701

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 |||
 317 GACGAGTGTTCACGACATAGTTACAGGTCGCTCTCCGACATGCC 366

17 a 17

```

367 T 367
seq_name: gb_est1:AA660952

seq_documentation_block:
LOCUS      AA660952      719 bp      mRNA      08-MAR-2000
DEFINITION 00849 MERHE Medicago truncatula cDNA 5', mRNA sequence.
ACCESSION  AA660952
VERSION    AA660952.1 GI:2604996
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 719)
AUTHORS   Covitz,P.A., Smith,L.S. and Long,S.R.
TITLE     Expressed sequence tags from a root-hair-enriched medicago
            truncatula cDNA library
JOURNAL   Plant Physiol. 117 (4), 1325-1332 (1998)
COMMENT   Contact: Long SR
            Department of Biological Sciences and Howard Hughes Medical
            Institute
            Stanford University
            Gilbert Biology, Stanford, CA 94305-5020, USA
            Tel: 650 723 3232
            Fax: 650 725 8309
            Email: fa.srl@leforsthe.stanford.edu
            Seq primer: T3.
            Location/Qualifiers
                1..719
                /organism="Medicago truncatula"
                /cultivar="Jemalong"
                /db_xref="taxon:3880"
                /clone_lib="MTRHE"
                /tissue_type="Root hairs & tips"
                /dev_stage="2-3 day old seedlings"
                /note="Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
                Site_2: XhoI; cDNA was synthesized from a pooled mRNA prep
                from elongating root hairs (30% w/w) and 2-3cm root tips
                (70% w/w). XhoI-oligo-dT linker-primer and EcoRI
                adaptors were used. cDNAs was cloned unidirectionally
                into lambda ZAP Express (Stratagene), amplified, and
                mass-exclused into pBK-CMV vector plasmids. More
                information is available at http://bio-srl@stanford.edu."
BASE COUNT  255 a 163 c 122 g 172 t
ORIGIN

alignment_scores:
    Quality: 78.00      Length: 17
    Ratio: 4.588        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x AA660952 ..
Align seg 1/1 to: AA660952 from: 1 to: 719
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
298 GACGAGTTGTTAGCAGCATAGGTTACAGGTTCCGCTCTCCGACATGCG 347

17 a 17
348 T 348
seq_name: gb_est2:BG647068

seq_documentation_block:
LOCUS      BG647068      748 bp      mRNA      EST      24-APR-2001
DEFINITION 00849 MERHE Medicago truncatula cDNA 5', mRNA sequence.
ACCESSION  BG647068
VERSION    BG647068.1 GI:13782180
KEYWORDS   EST.
SOURCE     barrel medic.
ORGANISM   Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
REFERENCE  1 (bases 1 to 748)
AUTHORS   Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
            Uterback,T., Cho,J. and Fraser,C.M.
TITLE     ESTs from roots of Medicago truncatula treated with
            oligogalacturonides of DP 6-20
JOURNAL   Unpublished (2001)
COMMENT   Contact: Michael G. Hahn
            Complex Carbohydrate Research Center
            University of Georgia
            220 Riverbend Road, Athens, GA 30602-4712, USA
            Tel: 706-542-4457
            Fax: 706-542-4412
            Email: hahn@ccrc.uga.edu
            G390574e TIGR sequence name: MTMBU48TK More information is
            available at: www.medicago.org
            Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
            Location/Qualifiers
                1..748
                /organism="Medicago truncatula"
                /cultivar="A17"
                /db_xref="taxon:3880"
                /clone_lib="phOGA-15H23"
                /tissue_type="3 day old seedling roots"
                /dev_stage="24 hours after treatment in the dark at 26 C
                with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
                presence of 100 ug/ml Gentamicin"
                /lab_host="XLOLR"
                /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
                was directionally ligated into the Unizap XR vector from
                Stratagene and packaged using Gigapack III Gold packaging
                extracts. Plasmids containing cDNA inserts were excised
                from the recombinant lambda-zap phage using Ex-assist
                helper phage and propagated in SOLR cells."
BASE COUNT  261 a 170 c 131 g 186 t
ORIGIN

alignment_scores:
    Quality: 78.00      Length: 17
    Ratio: 4.588        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 94.118

alignment_block:
US-09-485-529-104 x BG647068 ..
Align seg 1/1 to: BG647068 from: 1 to: 748
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
327 GACGAGTTGTTAGCAGCATAGGTTACAGGTTCCGCTCTCCGACATGCG 376

17 a 17
377 T 377
seq_name: gb_est2:BG440209

seq_documentation_block:
LOCUS      BG440209      684 bp      mRNA      EST      15-MAR-2001
DEFINITION GA_Ea0006G06f Gossypium arboreum 7-10 dpa fiber library Gossypium

```

arborescence cDNA clone GA_Ea0006G06f, mRNA sequence.
 BG440209
 VERSION BG440209.1 GI:13349859
 KEYWORDS EST.
 SOURCE Gossypium arboreum.
 ORGANISM Gossypium arboreum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 684)
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
 An integrated analysis of the genetics, development, and evolution of the cotton fiber
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Seq primer: TAATACGACTCTACTATAGG
 High quality sequence stop: 682.
 Location/Qualifiers
 1..684
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone_lib="GA_Ea0006G06f"
 /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
 /tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
 /lab_host="E. coli"
 /note="Vector: PBK-CMV; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 205 a 145 c 138 g 196 t
 ORIGIN

alignment_scores
 Quality: 74.00 Length: 17
 Ratio: 4.353 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 88.235

alignment_block
 US-09-485-529-104 x BG440209 ..
 Align seg 1/1 to: BG440209 from: 1 to: 684

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 229 GACGAGTTTACGCTGTTTGGTTACAAAGTCGGTCATCAGATATGCC 278
 17 a 17
 279 G 279

seq_name: gb_est1:AW584431

seq_documentation_block:
 LOCUS AW584431 712 bp mRNA EST 07-SEP-2000
 DEFINITION N210477E MHAM Medicago truncatula/Glomus versiforme mixed EST
 library cDNA clone MHAM-2017, mRNA sequence.
 ACCESSION AW584431
 VERSION AW584431.1 GI:7261485
 KEYWORDS EST.
 SOURCE Medicago truncatula/Glomus versiforme mixed EST library.
 ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.
 Eukaryota; mixed EST libraries.
 1 (bases 1 to 712)
 Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

ESTs from roots of Medicago truncatula after colonization with Glomus versiforme
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Harrison M.J.
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73401
 Tel: 580-223-5810
 Fax: 580-221-7380
 Email: mjharrison@noble.org
 Other name: MHAM-2a-H09; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chryslie.tamu.edu/medicago'.
 Seq primer: r3.
 Location/Qualifiers
 1..712
 /organism="Medicago truncatula/Glomus versiforme mixed EST library"
 /cultivar="Medicago truncatula genotype A17"
 /db_xref="taxon:119092"
 /clone_lib="MHAM-2017"
 /clone_lib="MHAM"
 /tissue_type="roots colonized with Glomus versiforme"
 /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
 /lab_host="E. coli strain XL0LR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in XL0LR cells."
 BASE COUNT 249 a 160 c 128 g 175 t
 ORIGIN

alignment_scores
 Quality: 74.00 Length: 17
 Ratio: 4.353 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 88.235

alignment_block
 US-09-485-529-104 x AW584431 ..
 Align seg 1/1 to: AW584431 from: 1 to: 712

1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 317 GACGAGTTTACGAGCATAGGTAGGTACAGGTTCCGCTCTCCGACATGCC 366
 17 a 17
 367 T 367

seq_name: gb_est1:AW688657

seq_documentation_block:
 LOCUS AW688657 651 bp mRNA EST 15-JUN-2000
 DEFINITION NF010B04ST1F1000 Developing stem Medicago truncatula cDNA clone
 NF010B04ST 5', mRNA sequence.
 ACCESSION AW688657
 VERSION AW688657.1 GI:7563393
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

```

REFERENCE 1 (bases 1 to 651)
AUTHORS   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
          C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
          R.A.
TITLE     Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL   Medicago truncatula stem library
COMMENT   Unpublished (2000)
          Contact: Dixon RA
          Plant Biology Division
          The Samuel Roberts Noble Foundation
          2510 Sam Noble Parkway, Ardmore, OK 73402, USA
          Tel: 580 221 7302
          Fax: 580 221 7380
          Email: radixon@noble.org
          Insert Length: 651 Std Error: 0.00
          Plate: 010 row: B column: 04
          Seq primer: TCACACAGGAACAGCTAGAC.
FEATURES  Location/Qualifiers
            1..651
             /organism="Medicago truncatula"
             /db_xref="taxon:3880"
             /clone="NF010B04ST"
             /clone_lib="Developing stem"
             /tissue_type="stem"
             /dev_stage="Pooled developmental"
             /note="Vector: Lambda Zap; Contains a mixture of
             internodal stem segments"
BASE COUNT 193 a 139 c 143 g 175 t 1 others
ORIGIN
alignment_scores
  Quality: 72.00 Length: 16
  Ratio: 4.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 93.750
alignment_block:
US-09-485-529-104 x AW688657 ..
Align seg 1/1 to: AW688657 from: 1 to: 651
2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetala 17
|||||
50 GAGTGTGTAGCAGCATAGGTACAGGTTCCGCTCCGACATGGCT 97
seq_name: gb_est1:AI495884
seq_documentation_block:
LOCUS     AI495884 311 bp mRNA EST 01-DEC-1999
DEFINITION sb17d07.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl004-9062 5' similar to TR:023643 O23643 RGA2 PROTEIN. [1] ;,
mRNA sequence.
ACCESSION AI495884
VERSION   AI495884.1 GI:4396887
KEYWORDS  EST.
SOURCE    soybean.
ORGANISM  Glycine max
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE 1 (bases 1 to 311)
AUTHORS   Shoemaker,R., Kelm,P., Vodkin,L., Erpelnding,J., Coryell,V., Khanna
          A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
          Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
          Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
          R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
          R., Waterston,R. and Willson,R.
          Public Soybean EST Project
          Unpublished (1999)
          Contact: Shoemaker R/Public Soybean EST Project
          Public Soybean EST Project
          Washington University School of Medicine

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
High quality sequence stop: 307.
FEATURES  Location/Qualifiers
            1..311
             /organism="Glycine max"
             /db_xref="taxon:3847"
             /clone="GENOME SYSTEMS CLONE ID: Gm-cl004-9062"
             /clone_lib="Gm-cl004"
             /tissue_type="root"
             /lab_host="XL10-Gold"
             /note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
             XhoI; Root cDNA. The mRNA was isolated from entire roots
             of 8 day old 'Williams' seedlings which were propagated on
             paper towels with distilled water. Stratagene's cDNA
             Synthesis Kit (catalog #200401) was used to synthesize the
             cDNA. First- strand synthesis was performed with 5-methyl
             dCTP, hence the ligated cDNA is hemimethylated.
             Stratagene's first-strand synthesis primer was used
             [GAGAGGAGAGAGAGAGAGACTAGTCGAG(T)-18]. After
             second-strand synthesis, the cDNA ends were 'polished'
             with clone Pfu DNA polymerase, ligated to EcoRI adapters,
             and phosphorylated. The XhoI site within the first-strand
             synthesis primer was restricted by digestion with XhoI;
             all XhoI sites in the cDNA would be protected by their
             hemimethylated status. The cDNA constructs were
             size-fractionated with a 500bp cutoff, using GibcoBRL Life
             Technologies' cDNA Size Fractionation column. The column
             eluent was then ligated into Stratagene's pBluescript II
             XR Predigested vector (pBluescript II SK(+)) that had been
             digested with EcoRI and XhoI, and phosphorylated). Both
             the white and blue colonies appear to contain recombinant
             plasmids with cDNA inserts. Blue colonies 9n-15) have been
             sequenced, and possess putative cDNA inserts. This library
             was constructed by Dr. Paul Keim & Virginia H. Coryell,
             Department of Biology, Box5640, Northern Arizona
             University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
             Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax:
             520-523-7500, email: paul.keim@nau.edu,
             virginia.coryell@nau.edu"
BASE COUNT 87 a 74 c 88 g 62 t
ORIGIN
alignment_scores
  Quality: 71.00 Length: 17
  Ratio: 4.176 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353
alignment_block:
US-09-485-529-104 x AI495884 ..
Align seg 1/1 to: AI495884 from: 1 to: 311
1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
115 GACGAGCTCTTCGAGTGGTGGGTACAGGTGAGGTGAGTGCATCGACATGCG 164
17 a 17
165 G 165
seq_name: gb_est1:AV409731
seq_documentation_block:

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LOCUS AV409731 365 bp mRNA EST 23-MAY-2000
 DEFINITION AV409731 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL061e11_r 5', mRNA sequence.
 ACCESSION AV409731
 VERSION AV409731.1 GI:7722585
 KEYWORDS EST.
 SOURCE Lotus japonicus.
 ORGANISM Lotus japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
 REFERENCE 1 (bases 1 to 365)
 AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
 TITLE Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
 JOURNAL DNA Res. 7 (2), 127-130 (2000)
 MEDLINE 20277479
 COMMENT Contact: Yasukazu Nakamura
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: ynakam@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
 FEATURES
 source
 1..365
 /organism="Lotus japonicus"
 /db_xref="taxon:34305"
 /clone="MWL061e11_r"
 /clone_lib="Lotus japonicus young plants (two-week old)"
 /dev_stage="young plants (two-week old)"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; Isolate=Miyakojima MG-20"
 XhoI
 BASE COUNT 106 a 95 c 102 g 62 t
 ORIGIN
 alignment_scores
 Quality: 71.00 Length: 17
 Ratio: 4.176 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 82.353
 alignment_block
 US-09-485-529-104 x AV409731 ..
 Align seg 1/1 to: AV409731 from: 1 to: 365
 1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
 |||||
 118 GAGGAGCTTCGCGTGGTGGTTACAAGGTGAGGTGCATCAGCATGGC 167
 17 a 17
 168 G 168
 seq_name: gb_est1:BE659954
 seq_documentation_block
 LOCUS BE659954 455 bp mRNA EST 06-SEP-2000
 DEFINITION 746 GmaxSC Glycine max cDNA, mRNA sequence.
 ACCESSION BE659954
 VERSION BE659954.1 GI:9985948
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 455)
 AUTHORS Harris,N., Chapman,B.P. and Gijzen,M.
 TITLE Gene expression in developing soybean seed coats
 JOURNAL Unpublished (2000)
 COMMENT Contact: Gijzen M

Agriculture and Agri-Food Canada
 1391 Sandford Street, London, Ontario, Canada N5V 4T3
 Tel: 519 457 1470
 Fax: 519 457 3997
 Email: gijzenm@agr.ca.
 Location/Qualifiers
 1..455
 /organism="Glycine max"
 /cultivar="Harosoy 63"
 /db_xref="taxon:3847"
 /clone_lib="GmaxSC"
 /tissue_type="Seed coats"
 /lab_host="E. coli strain XL0LR"
 /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developmental stage, average fresh weight 250 mg per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT) linker-primer. EcoRI adapters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amplified once using E. coli host strain XL1 Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host strain XL0LR."
 BASE COUNT 104 a 115 c 113 g 122 t 1 others
 ORIGIN
 alignment_scores
 Quality: 71.00 Length: 16
 Ratio: 4.438 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 93.750
 alignment_block
 US-09-485-529-104 x BE659954 ..
 Align seg 1/1 to: BE659954 from: 1 to: 455
 2 GluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
 :::
 332 AAGTTGCTGGCGGCTGGGTACAAGTTGCTGCTCCGACATGCC 379
 seq_name: gb_est2:BF424878
 seq_documentation_block
 LOCUS BF424878 465 bp mRNA EST 28-NOV-2000
 DEFINITION su52b08.y1 Gm-c1069 Glycine max cDNA clone GENOME SYSTEMS. CLONE ID: Gm-c1069-471 5' similar to TR:023642 O23642 RCAL PROTEIN. [1] ; , mRNA sequence.
 ACCESSION BF424878
 VERSION BF424878.1 GI:11412867
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 465)
 AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann ,R., Waterston,R. and Wilson,R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine,

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com

High quality sequence stop: 412.

FEATURES

source
1. .465
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl069-471"
/clone_lib="Gm-cl069"
/tissue_type="degenerating cotyledons, 9-10 day old etiolated seedling"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated seedlings for the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT 120 a 116 c 137 g 92 t
ORIGIN
alignment_scores:
Quality: 71.00 Length: 17
Ratio: 4.176 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353
alignment_block:
US-09-485-529-104 x BF424878 ..

Align seg 1/1 to: BF424878 from: 1 to: 465

1 AspCluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
114 GACGAGCTTCTCGGTGGTGTACAGGTTAGGTCATCGGACATGCG 163

17 a 17

164 G 164

seq_name: gb_est1:AW720697

seq_documentation_block:
LOCUS AW720697 478 bp mRNA EST 19-APR-2000
DEFINITION LjNEST/h8rc Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA 5', mRNA sequence.

ACCESSION AW720697

VERSION AW720697.1 GI:7615248

KEYWORDS EST.

SOURCE Lotus japonicus.

ORGANISM Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

REFERENCE 1 (bases 1 to 478)

AUTHORS Colebatch,G., Freund,S., Trevaskis,B and Udvardi,M.

TITLE Lotus japonicus root nodule ESTs: tools for functional genomics

JOURNAL Unpublished (2000)

COMMENT

Contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muehlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
Seq primer: T7
High quality sequence stop: 478.

FEATURES

source
1. .478
/organism="Lotus japonicus"
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and 7 week-old"
/dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI; Site_2: NotI; The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."

BASE COUNT 152 a 127 c 122 g 77 t
ORIGIN

alignment_scores:

Quality: 71.00 Length: 17
Ratio: 4.176 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x AW720697 ..

Align seg 1/1 to: AW720697 from: 1 to: 478

1 AspCluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
172 GACGAGCTTCTCGGTGGTGTACAGGTCATCGACATGCG 221

17 a 17

222 G 222

seq_name: gb_est2:BI419686

seq_documentation_block:

LOCUS BI419686 586 bp mRNA EST 15-AUG-2001
DEFINITION LjNEST47e12r Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA 5', mRNA sequence.

ACCESSION BI419686

VERSION BI419686.1 GI:15190709

KEYWORDS EST.

SOURCE Lotus japonicus.

ORGANISM Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

REFERENCE 1 (bases 1 to 586)

AUTHORS Colebatch,G., Freund,S., Trevaskis,B and Udvardi,M.

TITLE Lotus japonicus root nodule ESTs: tools for functional genomics

JOURNAL Unpublished (2000)

COMMENT Contact: Udvardi MK

Molecular Plant Nutrition

Max Planck Institute of Molecular Plant Physiology

Am Muehlenberg 1, 14476 Golm, Germany

Fax: 49 331 567 8250

Email: udvardi@mpimp-golm.mpg.de

Seq primer: T7

High quality sequence stop: 586.

Location/Qualifiers

1. .586

/organism="Lotus japonicus"

```

/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and 7
week-old"
/dev_stage="5 and 7 week-old plants"
/note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."
BASE COUNT      149 a 173 c 161 g 103 t
ORIGIN

alignment_scores:
  Quality: 71.00      Length: 17
  Ratio: 4.176       Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:
US-09-485-529-104 x BI419686 ..
Align seg 1/1 to: BI419686 from: 1 to: 586

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
119 GACGAGCTCTCGCGGTGGTGGGTACAGGTGAGGTGATCAGCATGGC 168

17 a 17
|
169 G 169

seq_name: gb_est1:AW267879

seq_documentation_block:
LOCUS AW267879 587 bp mRNA EST 07-SEP-2000
DEFINITION AW267879 DSIR Medicago truncatula cDNA clone pDSIR-8K8, mRNA
sequence.
ACCESSION AW267879.1 GI:6654835
VERSION AW267879
KEYWORDS barrel medic.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 587)
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng
,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Holt,I.E. and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula after inoculation with
Phytophthora medicaginis
JOURNAL Unpublished (1999)
COMMENT Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 612 625 5715
Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M250388e
TIGR sequence name:MTBAF64PK
More information, including clone ordering, is available at.
http://chrystle.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gTg gAT CC).
Location/Qualifiers
1..587
/organism="Medicago truncatula"
/cultivar="genotype Al7"
/db_xref="taxon:3880"
/clone="pDSIR-8K8"
/clone_lib="DSIR"

/tissue_type="roots infected with Phytophthora
medicaginis"
/dev_stage="roots harvested at 10 days post inoculation
with Phytophthora medicaginis"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10 days post inoculation with
Phytophthora medicaginis. The cDNA was directionally
ligated into the Uni-ZAP XR vector from Stratagene and
packaged using Gigapack III Gold packaging extracts. The
Plasmids containing cDNA inserts were excised from the
recombinant lambda-ZAP phage using Ex-Assist helper phage
and propagated in XL0LR cells. Note: EST may be of fungal
origin."
BASE COUNT      168 a 129 c 127 g 163 t
ORIGIN

alignment_scores:
  Quality: 71.00      Length: 17
  Ratio: 4.438       Gaps: 0
Percent Similarity: 94.118 Percent Identity: 88.235

alignment_block:
US-09-485-529-104 x AW267879 ..
Align seg 1/1 to: AW267879 from: 1 to: 587

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
3 GACGAGTTGTTAGCAGCATTAGGTTACAGGTTCTCTCTCCGACATGGC 52

17 a 17
|
53 T 53

seq_name: gb_est1:BE524828

seq_documentation_block:
LOCUS BE524828 374 bp mRNA EST 19-MAR-2001
DEFINITION M54G7STM Arabidopsis developing seed Arabidopsis thaliana cDNA
clone M54G7 5', mRNA sequence.
ACCESSION BE524828
VERSION BE524828.1 GI:9782806
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 374)
AUTHORS White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
Ilarduya,O., Jaworski,J.G., Ohlrogge,J. and Benning,C.
TITLE A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
JOURNAL Plant Physiol. 124 (4), 1582-1594 (2000)
MEDLINE 20567808
COMMENT Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
Location/Qualifiers
1..374
/organism="Arabidopsis thaliana"
source
FEATURES

```

```

/strain="Columbia"
/db_xref="taxon:3702"
/clone="M54G7"
/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoII"
BASE COUNT 97 a 88 c 87 g 102 t
ORIGIN

alignment_scores:
  Quality: 70.00 Length: 17
  Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:
US-09-485-529-104 x BE524828 ..
Align seg 1/1 to: BE524828 from: 1 to: 374
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
100 GATGAGCTTCTGCTGTCTTGGCTACAAGGTCGATCTTCTGAGATGCC 149

17 a 17
150 T 150

seq_name: gb_est2:T22782
seq documentation_block:
LOCUS T22782 457 bp mRNA EST 06-NOV-1997
DEFINITION 4790 Lambda-PRL2 Arabidopsis thaliana cDNA clone 107E8T7, mRNA
sequence.
ACCESSION T22782
VERSION T22782.1 GI:2597312
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 457)
AUTHORS Newman,T., deBrujin,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel
,E. and Somerville,C.
TITLE Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL Plant Physiol. 106, 1241-1255 (1994)
MEDLINE 95148729
COMMENT On Nov 6, 1997 this sequence version replaced gi:932620.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
FEATURES
  source
    Location/Qualifiers
      1..457
        /organism="Arabidopsis thaliana"
        /strain="var columbia"
        /db_xref="taxon:3702"
        /clone="107E8T7"
        /clone_lib="Lambda-PRL2"
        /note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
        Lambda PRL2 is a cDNA library derived from equal
        quantities of 4 pools of mRNA. The mRNA sources were 1) 7
        day germinated etiolated seedlings; 2) tissue culture
        grown roots; 3) staged plants half with 24 hour light
        cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
        same plants as 3 but aerial tissue (stems, flowers and
        siliques. The vector is BRL's lambda Zip-Lox. The cDNA
        inserts were directionally cloned with Sal-Not arms using
        oligo dt primed cDNA."
BASE COUNT 141 a 86 c 87 g 125 t 18 others
ORIGIN

alignment_scores:
  Quality: 70.00 Length: 17
  Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:
US-09-485-529-104 x T22782 ..
Align seg 1/1 to: T22782 from: 1 to: 457
1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
256 GATGAGCTTCTGCTGTCTTGGTATAAGGTTAGGTCATCCGAATGCC 305

17 a 17
306 T 306

seq_name: gb_est1:AV526467
seq documentation_block:
LOCUS AV526467 545 bp mRNA EST 01-SEP-2000
DEFINITION AV526467 Arabidopsis thaliana aboveground organs two to six-week
old Arabidopsis thaliana cDNA clone APZ14e05R 5', mRNA sequence.
ACCESSION AV526467
VERSION AV526467.1 GI:8685995
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 545)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
JOURNAL DNA Res. 7, 175-180 (2000)
MEDLINE 20363093
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
  source
    Location/Qualifiers
      1..545
        /organism="Arabidopsis thaliana"
        /strain="Columbia"
        /db_xref="taxon:3702"
        /clone="APZ14e05R"
        /clone_lib="Arabidopsis thaliana aboveground organs two to
        six-week old"
        /tissue_type="aboveground organs"
        /dev_stage="two to six-week old"
        /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
        XhoI"
BASE COUNT 151 a 120 c 132 g 142 t
ORIGIN

alignment_scores:
  Quality: 70.00 Length: 17

```

Ratio: 4.118 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x AV526467 ..

Align seg 1/1 to: AV526467 from: 1 to: 545

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
188 GATGAGCTCTTCTGCTCTTGGCTACAAAGGTCGATCTCTGAGATGCC 237

17 a 17

238 T 238

seq_name: gb_est2:BG442853

seq_documentation_block: 655 bp mRNA EST 15-MAR-2001
LOCUS BG442853
DEFINITION GA_Ea0018120f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0018120f, mRNA sequence.
ACCESSION BG442853
VERSION BG442853.1 GI:13352505
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 655)

Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
unpublished (2000)

CONTACT: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGG

High quality sequence stop: 647.

FEATURES

source

1..655

/organism="Gossypium arboreum".

/strain="AKA"

/cultivar="8400"

/db_xref="taxon:29729"

/clone="GA_Ea0018120f"

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

/tissue_type="Fibers isolated from bolls harvested 7-10

dp"

/lab_host="E. coli"

/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT

165 a 188 c 132 g 170 t

ORIGIN

alignment_scores:

Quality: 70.00 Length: 17

Ratio: 4.118 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 82.353

alignment_block:

US-09-485-529-104 x BG442853 ..

Align seg 1/1 to: BG442853 from: 1 to: 655

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||

195 GATGAGCTTTTGGCGGTTTTGGTTTACAAGGTCAAACCTTCAGACATGCC 244

17 a 17

245 T 245

seq_name: gb_est2:BI267918

seq_documentation_block: 227 bp mRNA EST 18-JUL-2001
LOCUS BI267918
DEFINITION NF112E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone
NF112E07IN 5', mRNA sequence.

ACCESSION BI267918

VERSION BI267918.1 GI:14873367

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

1 (bases 1 to 227)

Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
, H.R., Inman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula insect herbivory library

unpublished (2000)

CONTACT: Korth K

Dept. of Plant Pathology

University of Arkansas

217 Plant Science Building, Fayetteville, AR 72701, USA

Tel: 501 575 5191

Fax: 501 575 7601

Email: kthor@comp.uark.edu

Insert Length: 227 Std Error: 0.00

Plate: 112 row: E column: 07

Seq primer: TCACACAGGAACAGCATATGAC.

FEATURES

source

1..227

/organism="Medicago truncatula"

/db_xref="taxon:3880"

/clone="NF112E07IN"

/clone_lib="insect herbivory"

/tissue_type="local and systemic leaves"

/dev_stage="mature"

/note="vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."

BASE COUNT 74 a 27 c 67 g 57 t 2 others

ORIGIN

alignment_scores:

Quality: 68.00 Length: 17

Ratio: 4.000 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x BI267918 ..

Align seg 1/1 to: BI267918 from: 1 to: 227

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||

144 GATGACTCTTAGCTGTAGTTGGTTACAAGTGAATCTTCAGACATGCC 193

17 a 17

194 T 194

seq_name: gb_est1:BE317531

seq_documentation_block: 288 bp mRNA EST 21-DEC-2000
 LOCUS BE317531
 DEFINITION NF051B06LFF1045 Developing leaf Medicago truncatula cDNA clone
 ACCESSION BE317531
 VERSION NF051B06LFF 5', mRNA sequence.
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 REFERENCE 1 (bases 1 to 288)
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
 Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula leaf library
 COMMENT On Jul 14, 2000 this sequence version replaced gi:9191308.
 CONTACT: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Medicago Genome Initiative accession: MGI:S:21598
 Insert Length: 766 Std Error: 0.00
 Plate: 051 row: B column: 06
 Seq primer: TCACACAGGAACAGCTATGAC.

FEATURES
 source
 1..288
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="NF051B06LFF"
 /clone_lib="Developing leaf"
 /tissue_type="leaf"
 /dev_stage="Pooled developmental"
 /note="Vector: Lambda Zap; Contains a mixture of very
 young, developing, mature and senescing leaves."

BASE COUNT 107 a 34 c 77 g 70 t
 ORIGIN
 alignment_scores:
 Quality: 68.00 Length: 17
 Ratio: 4.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:
 US-09-485-529-104 x BE317531 ..

Align seg 1/1 to: BE317531 from: 1 to: 288

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 175 GATGAACCTTAGCTAGTGGTTACAAAGTGAATCTTCAGACATGGC 224

17 a 17
 |
 225 T 225

seq_name: gb_est1:AL371416

seq_documentation_block:
 LOCUS AL371416 398 bp mRNA EST 03-AUG-2000
 DEFINITION MTBA44A11F1 MTBA Medicago truncatula cDNA clone MTBA44A11 T3, mRNA
 sequence.
 ACCESSION AL371416
 VERSION AL371416.1 GI:9671169
 KEYWORDS EST.

SOURCE

ORGANISM
 barrel medic.
 Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE 1 (bases 1 to 398)
 AUTHORS Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
 Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
 V. and Gamas, P.

TITLE Medicago truncatula ESTs from nitrogen-starved roots
 JOURNAL Unpublished (2000)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
 Biologie Moleculaire des Relations Plantes-Microorganismes,
 CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
 Mt-est@toulouse.inra.fr Website:
 http://sequence.toulouse.inra.fr/Mtruncatula.html).

FEATURES
 Location/Qualifiers
 source
 1..398

/organism="Medicago truncatula"
 /cultivar="Jemalong"
 /db_xref="taxon:3880"
 /clone="MTBA44A11"
 /clone_lib="MTBA"
 /tissue_type="root tips"
 /dev_stage="harvested after 3 days of N-starvation"
 /note="Vector: pBluescript PSK; Site 1: EcoRI; Site 2:
 XhoI; Plants were grown in an aeroponic chamber for 14
 days on nitrogen-rich medium followed by 3 days on N-free
 medium. RNA was extracted from root tips (1-3 cm). cDNA
 was prepared from polyA+ enriched RNA. The cDNA was
 directionally ligated into Uni-zapXR vector from
 Stratagene and packaged using Gigapack Gold packaging
 extracts. Plasmids containing cDNA inserts were
 mass-excised from phage stocks using ExAssit helper phage
 and propagated in SOLR cells. Clone ordering and
 sequencing was performed by the Centre National de
 Sequencage (Genoscope, Evry, France)."

BASE COUNT 140 a 69 c 88 g 101 t
 ORIGIN
 alignment_scores:
 Quality: 68.00 Length: 17
 Ratio: 4.000 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:
 US-09-485-529-104 x AL371416 ..

Align seg 1/1 to: AL371416 from: 1 to: 398

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
 |||||
 178 GATGAACCTTAGCTAGTGGTTACAAAGTGAATCTTCAGACATGGC 227

17 a 17
 |
 228 T 228

seq_name: gb_est2:BI267177

seq_documentation_block:
 LOCUS BI267177 442 bp mRNA EST 18-JUL-2001
 DEFINITION NF102E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone
 NF102E07IN 5', mRNA sequence.
 ACCESSION BI267177
 VERSION BI267177.1 GI:14871977
 KEYWORDS EST.

SOURCE
ORGANISM
barrel medic.
Medicago truncatula

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

JOURNAL
COMMENT
1 (bases 1 to 442)
Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores
H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

FEATURES
source
1..442
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF102E07IN"
/clone_lib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully
expanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
BASE COUNT 154 a 81 c 93 g 112 t 2 others
ORIGIN

alignment_scores
Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block
US-09-485-529-104 x B1267177 ..
17 a 17
236 T 236

Align seg 1/1 to: B1267177 from: 1 to: 442

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
186 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAAATCTTCAGACATGCC 235

17 a 17
236 T 236

seq_name: gb_est2:BF634231

seq_documentation_block:
LOCUS BF634231 454 bp mRNA EST 19-DEC-2000
DEFINITION :NF084H12DTrF1103 Drought Medicago truncatula cDNA clone NF084H12DT
5', mRNA sequence.

ACCESSION | BF634231
VERSION BF634231.1 GI:11899389
KEYWORDS
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE
1 (bases 1 to 454)

AUTHORS
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

JOURNAL
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 454 Std Error: 0.00
Plate: 084 row: H column: 12
Seq primer: TCACACAGGAACACAGCTATGAC.
Location/Qualifiers
1..454
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF084H12DT"
/clone_lib="Drought"
/tissue_type="Plantlets"
/dev_stage="pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
timepoints."
BASE COUNT 150 a 92 c 96 g 115 t 1 others
ORIGIN

alignment_scores
Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block
US-09-485-529-104 x BF634231 ..
17 a 17
208 T 208

Align seg 1/1 to: BF634231 from: 1 to: 454

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
158 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAAATCTTCAGACATGCC 207

17 a 17
208 T 208

seq_name: gb_est1:AW691269

seq_documentation_block:
LOCUS AW691269 470 bp mRNA EST 21-DEC-2000
DEFINITION :NF039G01ST1F1000 Developing stem Medicago truncatula cDNA clone
NF039G01ST 5', mRNA sequence.

ACCESSION AW691269
VERSION AW691269.2 GI:11957372
KEYWORDS
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE
1 (bases 1 to 470)
He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
R.A.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)

JOURNAL
COMMENT
On Apr 14, 2000 this sequence version replaced gi:7566005.
Contact: Dixon RA
Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 678 Std Error: 0.00
Plate: 039 row: G column: 01
Seq primer: TCACACAGGAACACGCTATGAC.

FEATURES

source
1. 470
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_lib="NF039G01St"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
BASE COUNT 151 a 98 c 98 g 123 t
ORIGIN

alignment_scores:

Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x AW691269 ..
Align seg 1/1 to: AW691269 from: 1 to: 470
1 AspCluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
160 GATGAACCTCTAGCTAGTGGTTACAAAGTGAATCTTCAGACATGGC 209

17 a 17

210 T 210

seq_name: gb_est1:BE202661

seq_documentation_block:

LOCUS BE202661 482 bp mRNA EST 07-SEP-2000
DEFINITION EST402683 KV1 Medicago truncatula cDNA clone pkV1-2B16, mRNA
sequence.
ACCESSION BE202661
VERSION BE202661.1 GI:8745925
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 482)
VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.

TITLE

ESTs from roots of Medicago truncatula 24 hours after inoculation

JOURNAL

with Sinorhizobium meliloti

COMMENT

Unpublished (1999)
Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M University: T262354e
TIGR sequence name: MTIAD08TK
More information is available at.
http://chrysie.tamu.edu/medicago

FEATURES

source
1. 482
/organism="Medicago truncatula"
/cultivar="genotype Al7"
/db_xref="taxon:3880"
/clone_lib="pKV1-2B16"
/clone_lib="KV1"
/tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
BASE COUNT 157 a 96 c 106 g 123 t
ORIGIN

alignment_scores:

Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x BE202661 ..
Align seg 1/1 to: BE202661 from: 1 to: 482
1 AspCluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
152 GATGAACCTCTAGCTAGTGGTTACAAAGTGAATCTTCAGACATGGC 201

17 a 17

202 T 202

seq_name: gb_est1:BE205231

seq_documentation_block:

LOCUS BE205231 495 bp mRNA EST 05-SEP-2000
DEFINITION EST397907 KV0 Medicago truncatula cDNA clone pkV0-21C7, mRNA
sequence.
ACCESSION BE205231
VERSION BE205231.1 GI:8748527
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 495)
VandenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.

TITLE

ESTs from uninoculated seedling roots of Medicago truncatula

JOURNAL

Unpublished (1999)

COMMENT

Contact: VandenBosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M University name: T265003e
TIGR sequence name: MTGBK16TK
More information is available at.
http://chrysie.tamu.edu/medicago

Seq primer: SKmod (CTA GAA CTA gTg gAT CC).

FEATURES

source

1. .495
/location="Qualifiers"
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV0-21C7"
/clone_lib="KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XL0LR"
/note="vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

BASE COUNT
ORIGIN

165 a 101 c 105 g 124 t

alignment_scores:

Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x BE205231 ..

Align seg 1/1 to: BE205231 from: 1 to: 495

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
162 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAATCTTCAGACATGCG 211

17 a 17

212 T 212

seq_name: gb_est1:BE205387

seq_documentation_block:

LOCUS BE205387 522 bp mRNA EST 05-SEP-2000
DEFINITION EST398063 KV0 Medicago truncatula cDNA clone pkV0-21B13, mRNA
sequence.

ACCESSION BE205387

VERSION BE205387.1 GI:8748684

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 522)
VandenBosch, K., Endre, G., Hurr, J., Moore, J., Beremand, P., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.

AUTHORS

ESTs from uninoculated seedling roots of Medicago truncatula

Unpublished (1999)

Contact: VandenBosch K

Department of Biology

Texas A&M University

College Station, TX 77843-3258, USA

Tel: 409 845 7707

Fax: 409 845 2891

Email: kate@mail.bio.tamu.edu

Texas A&M University name: T265159e

TIGR sequence name: MTGDM07TK

More information is available at...

<http://chrystie.tamu.edu/medicago>

Seq primer: SKmod (CTA GAA CTA gTg gAT CC).

FEATURES

source

1. .522
/location="Qualifiers"
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pkV0-21B13"
/clone_lib="KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XL0LR"
/note="vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-zap phage using Ex-assist
helper phage and propagated in XL0LR cells."

BASE COUNT
ORIGIN

162 a 112 c 110 g 138 t

alignment_scores:

Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x BE205387 ..

Align seg 1/1 to: BE205387 from: 1 to: 522

1 AspGluLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
|||||
98 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAATCTTCAGACATGCG 147

17 a 17

148 T 148

seq_name: gb_est1:AW684591

seq_documentation_block:

LOCUS AW684591 544 bp mRNA EST 15-JUN-2000
DEFINITION NF018F10NR1F1000 Nodulated root Medicago truncatula cDNA clone
NF018F10NR 5', mRNA sequence.

ACCESSION AW684591

VERSION AW684591.1 GI:7559327

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 544)
Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R.,
Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May,
G.D. and Paiva, N.L.

AUTHORS

Expressed Sequence Tags from the Samuel Roberts Noble Foundation

Medicago truncatula nodulated root library

Unpublished (2000)

Contact: Paiva NL

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7317

Fax: 580 221 7380

Email: nlpaiva@noble.org

Insert Length: 544 Std Error: 0.00

Plate: 018 row: F column: 10

Seq primer: TCACACGGAACACGCTATGAC.


```

FEATURES
  source
    Location/Qualifiers
      1..544
        /organism="Medicago truncatula"
        /db_xref="taxon:3880"
        /clone="NF018F10NR"
        /clone_lib="Modulated root"
        /tissue_type="root"
        /dev_stage="Pooled developmental"
        /note="Vector: Lambda Zap; Four-week old Rhizobium
        meliloti-inoculated Medicago truncatula roots, containing
        a mixture of young and old roots and nodules."
BASE COUNT      185 a 115 c 107 g 133 t 4 others
ORIGIN

alignment_scores:
  Quality: 68.00      Length: 17
  Ratio: 4.000       Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:
  US-09-485-529-104 x AW684591 ..
    Align seg 1/1 to: AW684591 from: 1 to: 544
      1 AspgLUleuLeuAlaAlaLeuGLyTYrLYsValArgAlaSerAspMetAl 17
      179 GATGAACCTCTTAGCTGTAGTTGGTTACAAAGTGAATCTTCAGACATGCC 228
      17 a 17
      229 T 229
    seq_name: gb_estl:AW693047

seq_documentation_block:
  LOCUS      AW693047      601 bp      mRNA      EST      21-DEC-2000
  DEFINITION NF059C03ST1F1020 Developing stem Medicago truncatula cDNA clone
  ACCESSION  AW693047
  VERSION    AW693047.2 GI:11935888
  KEYWORDS   EST.
  SOURCE      barrel medic.
  ORGANISM   Medicago truncatula
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
              Medicago.
  REFERENCE  1 (bases 1 to 601)
  AUTHORS    He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
              ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
              ,R.A.
  TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
              Medicago truncatula stem library
  JOURNAL    Unpublished (2000)
  COMMENT    On Apr 14, 2000 this sequence version replaced gi:7567783.
              Contact: Dixon RA
              Plant Biology Division
              The Samuel Roberts Noble Foundation
              2510 Sam Noble Parkway, Ardmore, OK 73402, USA
              Tel: 580 221 7302
              Fax: 580 221 7380
              Email: radixon@noble.org
              Insert Length: 653 Std Error: 0.00
              Plate: 059 row: C column: 03
              Seq primer: TCACACAGGAACAGCATGAC.
              Location/Qualifiers
                1..601
                  /organism="Medicago truncatula"
                  /db_xref="taxon:3880"
                  /clone="NF059C03ST"
                  /clone_lib="Developing stem"
                  /tissue_type="stem"

FEATURES
  source
    Location/Qualifiers
      1..601
        /organism="Medicago truncatula"
        /db_xref="taxon:3880"
        /clone="NF059C03ST"
        /clone_lib="Developing stem"
        /tissue_type="stem"

```

```

/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
BASE COUNT      200 a 120 c 128 g 153 t
ORIGIN

alignment_scores:
  Quality: 68.00      Length: 17
  Ratio: 4.000       Gaps: 0
  Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:
  US-09-485-529-104 x AW693047 ..
    Align seg 1/1 to: AW693047 from: 1 to: 601
      1 AspgLUleuLeuAlaAlaLeuGLyTYrLYsValArgAlaSerAspMetAl 17
      175 GATGAACCTCTTAGCTGTAGTTGGTTACAAAGTGAATCTTCAGACATGCC 224
      17 a 17
      225 T 225
    seq_name: gb_estl:AW697328

seq_documentation_block:
  LOCUS      AW697328      613 bp      mRNA      EST      21-DEC-2000
  DEFINITION NF115E11ST1F1086 Developing stem Medicago truncatula cDNA clone
  ACCESSION  AW697328
  VERSION    AW697328.2 GI:11957114
  KEYWORDS   EST.
  SOURCE      barrel medic.
  ORGANISM   Medicago truncatula
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
              Medicago.
  REFERENCE  1 (bases 1 to 613)
  AUTHORS    He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
              ,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
              ,R.A.
  TITLE      Expressed Sequence Tags from the Samuel Roberts Noble Foundation
              Medicago truncatula stem library
  JOURNAL    Unpublished (2000)
  COMMENT    On Apr 14, 2000 this sequence version replaced gi:7572090.
              Contact: Dixon RA
              Plant Biology Division
              The Samuel Roberts Noble Foundation
              2510 Sam Noble Parkway, Ardmore, OK 73402, USA
              Tel: 580 221 7302
              Fax: 580 221 7380
              Email: radixon@noble.org
              Insert Length: 653 Std Error: 0.00
              Plate: 115 row: E column: 11
              Seq primer: TCACACAGGAACAGCATGAC.
              Location/Qualifiers
                1..613
                  /organism="Medicago truncatula"
                  /db_xref="taxon:3880"
                  /clone="NF115E11ST"
                  /clone_lib="Developing stem"
                  /tissue_type="stem"
                  /dev_stage="Pooled developmental"
                  /note="Vector: Lambda Zap; Contains a mixture of
                  internodal stem segments"
BASE COUNT      202 a 123 c 131 g 157 t
ORIGIN

alignment_scores:

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Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x AW697328 ..

Align seg 1/1 to: AW697328 from: 1 to: 613

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
|||||
183 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAATCTTCAGACATGCG 232

17 a 17

233 T 233

seq_name: gb_est1:AW690574

seq_documentation_block: 614 bp mRNA EST 15-JUN-2000
LOCUS AW690574
DEFINITION NF031C08S1F1000 Developing stem Medicago truncatula cDNA clone
NF031C08ST 5', mRNA sequence.

ACCESSION AW690574
VERSION AW690574.1 GI:7565310
KEYWORDS EST.
SOURCE barrel medic.

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE

1 (bases 1 to 614)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
,R.A.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library

JOURNAL

Unpublished (2000)

COMMENT

Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 614 Std Error: 0.00

Plate: 031 row: C column: 08

Seq primer: TCACACAGGAACAGCTATGAC.

Location/Qualifiers

FEATURES

source
1..614
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF031C08ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

BASE COUNT

183 a 130 c 126 g 170 t 5 others

ORIGIN

alignment_scores:
Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x AW690574 ..

Align seg 1/1 to: AW690574 from: 1 to: 614

1 AspGluLeuAlaLeuGlyTyrLysValArgAlaSerAspMetal 17
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38 GATGAACCTCTAGCTAGTGTGTTACAAAGTGAATCTTCAGACATGCG 87

17 a 17

88 T 88

seq_name: gb_est1:AW690601

seq_documentation_block: 620 bp mRNA EST 20-DEC-2000
LOCUS AW690601
DEFINITION NF036C12ST1F1000 Developing stem Medicago truncatula cDNA clone
NF036C12ST 5', mRNA sequence.

ACCESSION AW690601

VERSION AW690601.2 GI:11933126

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

1 (bases 1 to 620)

He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
,R.A.

TITLE

Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library

JOURNAL

Unpublished (2000)

COMMENT

On Apr 14, 2000 this sequence version replaced gi:7565337.

Contact: Dixon RA

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7302

Fax: 580 221 7380

Email: radixon@noble.org

Insert Length: 649 Std Error: 0.00

Plate: 036 row: C column: 12

Seq primer: TCACACAGGAACAGCTATGAC.

Location/Qualifiers

1..620
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/clone="NF036C12ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"

BASE COUNT 205 a 122 c 133 g 160 t

ORIGIN

alignment_scores:
Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471

alignment_block:

US-09-485-529-104 x AW690601 ..

Align seg 1/1 to: AW690601 from: 1 to: 620

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17 a 17

240 T 240

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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-235-836C-35+	32.00	100.00	639.97	624	!	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-671-817A-1+	32.00	84.34	4.8e+03	2990
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-506-553C-22-	32.00	99.58	675.69	651	!	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-149-100-1+	32.00	84.23	4.8e+03	3024
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-434-255-9+	32.00	99.16	713.16	679	!	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-671-817A-3+	32.00	84.09	4.9e+03	3066
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-460-327-9+	32.00	99.16	713.16	679	!	/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-694-824-23+	32.00	83.66	5.2e+03	3200
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-871-6+	32.00	99.16	713.16	679	!	/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-453-104-22+	32.00	83.66	5.2e+03	3201
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-459-871-6+	32.00	99.10	718.55	683	!	/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-694-824-22+	32.00	83.66	5.2e+03	3202
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-328-1161-695+	32.00	99.90	728.01	760	!	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-062-676B-1+	32.00	83.30	5.5e+03	3319
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-198-959A-9+	32.00	95.21	1.2e+03	1008	!	/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-349-867-18+	32.00	82.87	5.8e+03	3465
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-754-282B-2-	32.00	90.74	2.1e+03	1576	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-906-769-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-906-616-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-817-793-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-639-075A-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-012-692-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-906-613-112+	32.00	90.72	2.1e+03	1580	!	/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27+	32.00	82.67	5.9e+03	3531
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- 32.00 74.14 1.7e+04 8298						/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-757-653-30 +	31.50	93.74	1.4e+03	969
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- 32.00 68.69 3.5e+04 14311						/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-254-359A-12 +	31.50	88.72	2.7e+03	1600
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-471-066B-11 +	31.50	93.81	1.4e+03	962	1	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-254-359A-21 +	31.50	84.26	4.8e+03	2502
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-484-956-11 +	31.50	93.81	1.4e+03	962	1	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-483-043-21 +	31.50	84.26	4.8e+03	2502
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-757-653-11 +	31.50	93.81	1.4e+03	962	1	/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-481-238-21 +	31.50	84.26	4.8e+03	2502
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; Patent No. 6307126
; GENERAL INFORMATION:
; APPLICANT: Harberd, Nicholas P
; APPLICANT: Peng, Jinrong
; APPLICANT: Carol, Pierre
; APPLICANT: Richards, Donald E
; TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
; FILE REFERENCE: 620-45
; CURRENT APPLICATION NUMBER: US/09/117,853
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: PCT/GB97/00390
; EARLIER FILING DATE: 1997-02-12
; EARLIER APPLICATION NUMBER: GB 9602796.6
; EARLIER FILING DATE: 1996-02-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-117-853-1
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; Patent No. 6046042
; GENERAL INFORMATION:
; APPLICANT: Meinhard HASSLACHER et al.
; TITLE OF INVENTION: (S)-HYDROXY-NITRILE-LYASE FROM HEVEA BRASILIENSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,256A
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 1553-Oz1112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-981-256A-4

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seq_documentation_block:
; Sequence 5, Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
; APPLICANT: Granneman, James G.
; APPLICANT: Lahners, Kristine N.
; APPLICANT: Rao, Donald D.
; TITLE OF INVENTION: @ @3-ADRENERGIC RECEPTOR PROTEIN AND DNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
; ADDRESSEE: MILTON
; STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,901
; FILING DATE: 19920720
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
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NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324 (WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDS
LOCATION: 51..1250
US-07-916-901-5

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seq_documentation_block:
Sequence 43, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-991-867B-43

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2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
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84 GAATTTATTGAAGCTCAAAGTTATCTGTAAAAAGCATCGAT 125

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq.US-07-991-867B-45

seq_documentation_block:
Sequence 45, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-544-332-45

alignment_scores:
Quality: 41.00 Length: 14
Ratio: 3.727 Gaps: 0
Percent Similarity: 78.571 Percent Identity: 64.286

alignment_block:
US-09-485-529-104 x US-08-544-332-45 ..
Align seg 1/1 to: US-08-544-332-45 from: 1 to: 235

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 15
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84 GAATTATTGAACGTCAAAGGTTATCTGTAAAGCATCCGAT 125

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-424-224-1

seq_documentation_block:
Sequence 1, Application US/08424224
Patent No. 5912173
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.
TITLE OF INVENTION: MURINE IL-2R CDNA AND
NUMBER OF INVENTIONS: 2
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MURINE
INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-1

alignment_scores:
Quality: 41.00 Length: 13
Ratio: 3.727 Gaps: 0
Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
US-09-485-529-104 x US-08-424-224-1/rev ..
Align seg 1/1 to reverse of: US-08-424-224-1 from: 1 to: 1608

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
||||| ||||| ||||| ||||| |||||
1409 GAGCTCCAGCACCTGGCTACAGGTAAGACTCTCT 1371

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-02891-68

seq_documentation_block:
Sequence 68, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: XSCID
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1608
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: MURINE
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-68

alignment_scores:

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Quality: 41.00      Length: 13
Ratio: 3.727       Gaps: 0
Percent Similarity: 84.615      Percent Identity: 69.231

alignment_block:
US-09-485-529-104 x PCT-US94-02891-68/rev ..

Align seg 1/1 to reverse of: PCT-US94-02891-68 from: 1 to: 1608

      2 GluLeuLeuAlaAlaLeuGlyTyrIysValArqAlaSer 14
      ||||| |||:::|||||:::|||||:::||||| |||
1409 GAGCTCCAGCCACCCCTGGCTACAGGGTAAGACTCTCT 1371

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-090-793-13

seq_documentation_block:
; Sequence 13, Application US/09090793
; Patent No. 6140486
; GENERAL INFORMATION:
; APPLICANT: Calgene, LLC
; TITLE OF INVENTION: Production of polyunsaturated fatty acids by
; FILE OF INVENTION: of polyketide-like synthesis genes in plants
; FILE REFERENCE: CGNE.131.01US
; CURRENT APPLICATION NUMBER: US/09/090.793
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048.650
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 19227
; TYPE: DNA
; ORGANISM: Vibrio marinus
US-09-090-793-13

alignment_scores:
Quality: 40.00      Length: 10
Ratio: 4.444       Gaps: 0
Percent Similarity: 90.000      Percent Identity: 80.000

alignment_block:
US-09-485-529-104 x US-09-090-793-13/rev ..

Align seg 1/1 to reverse of: US-09-090-793-13 from: 1 to: 19227

      2 GluLeuLeuAlaAlaLeuGlyTyrIysVal 11
      |||||::: |||||:::|||||:::|||||
13732 GAACGTGATCTTGCCTTGGGTATAAAGTC 13703

seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-090-793-12

seq_documentation_block:
; Sequence 12, Application US/09090793
; Patent No. 6140486
; GENERAL INFORMATION:
; APPLICANT: Calgene, LLC
; TITLE OF INVENTION: Production of polyunsaturated fatty acids by
; FILE OF INVENTION: of polyketide-like synthesis genes in plants
; FILE REFERENCE: CGNE.131.01US
; CURRENT APPLICATION NUMBER: US/09/090.793
; CURRENT FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048.650
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 40138
; TYPE: DNA
; ORGANISM: Vibrio marinus
US-09-090-793-12

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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-31
seq_documentation_block:
; Sequence 31, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murty, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 703 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT01
; CLONE: 713784
; US-09-276-531-31

alignment_scores:
; Quality: 39.00 Length: 10
; Ratio: 3.900 Gaps: 0
; Percent Similarity: 100.000 Percent Identity: 70.000

seq_documentation_block:
; US-09-485-529-104 x US-09-276-531-31
; Align seg 1/1 to: US-09-276-531-31 from: 1 to: 703
; 1 AspGluLeuLeuAlaLeuGlyTyrIys 10
; :|||||
; 424 GAGCAGCTGCTGGCGCCTGGCTACGC 453
; seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-3
seq_documentation_block:
; Sequence 3, Application US/08087772A
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; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,772A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Linker, Raymond O.
; REGISTRATION NUMBER: 26,419
; REFERENCE/DOCKET NUMBER: 3339-195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-087-772A-3

alignment_scores:
; Quality: 39.00 Length: 13
; Ratio: 3.545 Gaps: 0
; Percent Similarity: 84.615 Percent Identity: 69.231

seq_documentation_block:
; US-09-485-529-104 x US-08-087-772A-3/rev
; Align seg 1/1 to reverse of: US-08-087-772A-3 from: 1 to: 1164
; 3 LeuLeuAlaAlaLeuGlyTyrIysValargAlaSerAsp 15
; :|||||
; 80 GTGTGGCTGCTGGGTCCAGGTCCAGGTGGCGTCCGAC 42
; seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-4
seq_documentation_block:
; Sequence 4, Application US/08087772A
; Patent No. 5691155
; GENERAL INFORMATION:
; APPLICANT: Nahmias, Clara
; APPLICANT: Emorine, Jean L.
; APPLICANT: Strosberg, Donny A.
; TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
; Beta3-Adrenergic Receptor and Their Applications
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691155th Carolina
; COUNTRY: USA
```

```
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3175
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-087-772A-4

alignment_scores:
Quality: 39.00 Length: 13
Ratio: 3.545 Gaps: 0
Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
US-09-485-529-104 x US-08-087-772A-4/rev ..
Align seg 1/1 to reverse of: US-08-087-772A-4 from: 1 to: 1360

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
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647 GTGTTGGTGCACCTGGGTCACGGGTAGGGCGTCCGAC 55

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-087-772A-1

seq_documentation_block:
Sequence 1, Application US/0808772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
```

```
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 568..1731
US-08-087-772A-1

alignment_scores:
Quality: 39.00 Length: 13
Ratio: 3.545 Gaps: 0
Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:
US-09-485-529-104 x US-08-087-772A-1/rev ..
Align seg 1/1 to reverse of: US-08-087-772A-1 from: 1 to: 1920

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
:::|||||
647 GTGTTGGTGCACCTGGGTCACGGGTAGGGCGTCCGAC 609

seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-450-962-3

seq_documentation_block:
Sequence 3, Application US/08450962
Patent No. 6274706
GENERAL INFORMATION:
APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
APPLICANT: STROSBERG, Donny
TITLE OF INVENTION: INTRON/EXON OF THE HUMAN AND
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: KECK, MAHIN & CATE
STREET: P.O. BOX 06110
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael A.
REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 3:
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SEQUENCE CHARACTERISTICS:

LENGTH: 3437 bases
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-450-962-3

alignment_scores:
 Quality: 39.00 Length: 13
 Ratio: 3.545 Gaps: 0
 Percent Similarity: 84.615 Percent Identity: 69.231

alignment_block:

US-09-485-529-104 x US-08-450-962-3/rev ..

Align seg 1/1 to reverse of: US-08-450-962-3 from: 1 to: 3437

3 LeuLeuAlaLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15

:::|||||:::|||||:::|||||:::|||||:::|||||

647 GTGTTGGTGCACCTGGGTCCAGGTAGGCGGTCCGAC 609

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-137-614A-3

seq_documentation_block:

Sequence 3, Application US/08137614A

Patent No. 5487976

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Knipple, Douglas C.

APPLICANT: Henderson, Joseph E.

TITLE OF INVENTION: Gene Encoding An Insect

TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,614A

FILING DATE: 15-OCT-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Timian, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/120

TELEPHONE: (716)263-1636

TELEFAX: (716)263-1600

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1491 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-137-614A-3

alignment_scores:

Quality: 38.00 Length: 16

Ratio: 3.455 Gaps: 0

Percent Similarity: 68.750 Percent Identity: 43.750

alignment_block:

US-09-485-529-104 x US-08-137-614A-3 ..

Align seg 1/1 to: US-08-137-614A-3 from: 1 to: 1491

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMet 16

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374 GAGACTTTTCTGAAAGATATGGGTACCGGATACGTTCTTCGCCAATG 421

seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-768-301-1

seq_documentation_block:

Sequence 1, Application US/08768301

Patent No. 5854002

GENERAL INFORMATION:

APPLICANT: Tomalski, Michael D.

APPLICANT: Gant, Daniel B.

TITLE OF INVENTION: METHOD OF IDENTIFYING COMPOUNDS THAT BIND

TITLE OF INVENTION: TO THE INSECT GABA RECEPTOR

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10112-0228

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/768,301

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: MacLeod, Janet M.

REGISTRATION NUMBER: 35,263

REFERENCE/DOCKET NUMBER: A30693

TELEPHONE: 212-408-2500

TELEFAX: 212-765-2519

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1491 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: CDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-768-301-1

alignment_scores:

Quality: 38.00 Length: 16

Ratio: 3.455 Gaps: 0

Percent Similarity: 68.750 Percent Identity: 43.750

alignment_block:

US-09-485-529-104 x US-08-768-301-1 ..

Align seg 1/1 to: US-08-768-301-1 from: 1 to: 1491

1 AspGluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAspMet 16

:::|||||:::|||||:::|||||:::|||||:::|||||

374 GAGACTTTTCTGAAAGATATGGGTACCGGATACGTTCTTCGCCAATG 421

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seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-799-464A-14
seq_documentation_block:
; Sequence 14, Application US/08799464A
; Patent No. 5998601
; GENERAL INFORMATION:
; APPLICANT: Murtaugh, Michael P. et al.
; TITLE OF INVENTION: VR-2332 VIRAL NUCLEOTIDE SEQUENCE AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins
; STREET: 2405 Grand Blvd., Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: USA
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,464A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/287,941
; FILING DATE: August 5, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 22907
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arteriviridae
; STRAIN: VR-2332
; FEATURE:
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; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /evidence= EXPERIMENTAL
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; FEATURE:
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; LOCATION: 13484..14089
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; NAME/KEY: misc feature
; LOCATION: 14588..14974
; OTHER INFORMATION: /standard_name= "LV ORF 7"
; OTHER INFORMATION: /citation= ({1})
; PUBLICATION INFORMATION:
; AUTHORS: Meulenbergh, J. J. M.
; AUTHORS: Hulst, M. M.
; AUTHORS: de Veijer, E. J.
; AUTHORS: Moonen, P. L.
; AUTHORS: den Besten, A.
; AUTHORS: de Kluyver, E. P.
; AUTHORS: Wensvoort, G.
; AUTHORS: Moormann, R. J.
; TITLE: Lelystad virus, the causative agent of
; TITLE: porcine epidemic abortion and respiratory
; TITLE: syndrome (PEARS) is related to LDV and EAV.
; JOURNAL: Virology
; VOLUME: 192
; PAGES: 62-72
; DATE: 1993
; RELEVANT RESIDUES IN SEQ ID NO: 14: FROM 1 TO 15101
; US-08-799-464A-14

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Ratio: 2.714 Gaps: 0
Percent Similarity: 93.333 Percent Identity: 46.667

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; Sequence 14, Application PC/TUS9509927
; GENERAL INFORMATION:
; APPLICANT: Murtaugh, Michael P.
; TITLE OF INVENTION: VR-2332 VIRAL NUCLEOTIDE SEQUENCE AND
; METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins
; STREET: 1101 Walnut, Suite 1400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: USA
; ZIP: 64106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09927
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26122
REFERENCE/DOCKET NUMBER: 22907
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15101 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arteriviridae
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FEATURE:
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IDENTIFICATION METHOD: experimental
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LOCATION: 14588..14974
OTHER INFORMATION: /standard_name= "LV ORF 7"
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PUBLICATION INFORMATION:
AUTHORS: Hulst, M. M.
AUTHORS: de Veijer, E. J.
AUTHORS: Moonen, P. L.
AUTHORS: den Besten, A.
AUTHORS: de Kluyver, E. P.
AUTHORS: Wensvoort, G.

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CITY: Salt Lake City
STATE: Utah
COUNTRY: USA
ZIP: 84111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS95
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/157,005
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Turner, Allen C.
REGISTRATION NUMBER: 33041
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 532-1922
TELEFAX: (801) 531-9188
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 212..7399
OTHER INFORMATION:
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NAME/KEY: CDS
LOCATION: 7384..11772
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LOCATION: 11786..12532
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NAME/KEY: CDS
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US-08-747-863-1

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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-614-770A-1

seq_documentation_block:
; Sequence 1, Application US/08614770A
; Patent No. 5773267
; GENERAL INFORMATION:
; APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
; TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
; STREET: 90 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
; MEDIUM TYPE: DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/614,770A
; FILING DATE: MARCH 7, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ELIZABETH A. BOGOSIAN
; REGISTRATION NUMBER: 39,911
; REFERENCE/DOCKET NUMBER: 96700/402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-5995
; TELEFAX: (212) 286-0854 or 286-0082
; TELEX: TWX 710-581-4766
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49272
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: OLIGONUCLEOTIDE
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIOPHAGE
; INDIVIDUAL ISOLATE: D29
US-08-614-770A-1

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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-955

seq_documentation_block:
; Sequence 955, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 955:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1590RP
US-08-998-416-955

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  Percent Similarity: 73.333  Percent Identity: 46.667

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362 CTGCTAAACTACTCGGTATCGAATCGGATTGCTACTTTAGCC 406
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Sequence 189, Application US/08998416
Patent No. 6239264


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; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGL1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 386:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAGI292UP
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; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippssen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
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/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10660)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6099
/ TELEFAX: (314)537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ TYPE: nucleic acid
/ LENGTH: 1377 base pairs
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-476-008-9

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Percent Similarity: 85.714 Percent Identity: 50.000

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seq_documentation_block:
/ Sequence 9, Application US/08306063
/ Patent No. 5633435
/ GENERAL INFORMATION:
/ APPLICANT: Barry, Gerard F.
/ APPLICANT: Kishore, Ganesh M.
/ APPLICANT: Padgett, Stephen R.
/ APPLICANT: Stallings, William C.
/ TITLE OF INVENTION: Glycosate Tolerant
/ TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
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/ APPLICATION NUMBER: US/08/306,063
/ FILING DATE: 13-SEP-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/749,611
/ FILING DATE: 28-AUG-1991
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/576,537
/ FILING DATE: 31-AUG-1990
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
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/ TELEPHONE: (314)537-6099
/ TELEFAX: (314)537-6047
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1377 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
US-08-306-063-9

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seq_documentation_block:
/ Sequence 14, Application US/08553943
/ Patent No. 5702933
/ GENERAL INFORMATION:
/ APPLICANT: Klee, Harry J.
/ APPLICANT: Kishore, Ganesh M.
/ TITLE OF INVENTION: Control of Fruit Ripening and Senescence
/ TITLE OF INVENTION: in Plants
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Monsanto Co. BB4F
/ STREET: 700 Chesterfield Village Parkway
/ CITY: St. Louis
/ STATE: Missouri
/ COUNTRY: USA
/ ZIP: 63198
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ APPLICATION NUMBER: US/08/553,943
/ FILING DATE: 06-NOV-1995
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/809,457
/ FILING DATE: 17-DEC-1991
/ APPLICATION NUMBER: US 07/632,440
/ FILING DATE: 26-DEC-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hoerner Jr., Dennis R.
/ REGISTRATION NUMBER: 30,914
/ REFERENCE/DOCKET NUMBER: 38-21(10538)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314)537-6099
/ TELEFAX: (314)537-6047
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1377 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
US-08-553-943-14

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seq_documentation_block:
; Sequence 9, Application US/08833485
; Patent No. 5804425
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgette, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,485
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

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US-08-833-485-9

alignment_scores:
  Quality: 37.00      Length: 14
  Ratio: 3.083        Gaps: 0
  Percent Similarity: 85.714  Percent Identity: 50.000

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1314 GATTGATGGCTGCTTGGAGCTAGATCGAAGTCTCCGAC 1355

seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-137-440-9

seq_documentation_block:
; Sequence 9, Application US/09137440
; Patent No. 6248876
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgette, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/137,440
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/833,485
; FILING DATE: 07-APR-1997
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(15117)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6099
; TELEFAX: (314)737-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-137-440-9

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alignment_scores:
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  Ratio: 3.083       Gaps: 0
  Percent Similarity: 85.714      Percent Identity: 50.000

alignment_block:
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Align seg 1/1 to: US-09-137-440-9 from: 1 to: 1377

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-06148A-9

seq_documentation_block:
; Sequence 9, Application PC/TUS9106148A
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; TITLE OF INVENTION: Glyphosate Tolerant
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06148A
; FILING DATE: 19910828
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10535)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1377 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US91-06148A-9

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  Percent Similarity: 85.714      Percent Identity: 50.000

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1314 GATTGATGGCTGCTTGGAGCTAAGATCGAACTCCGAC 1355

seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-09437-14

seq_documentation_block:
; Sequence 14, Application PC/TUS9109437
; GENERAL INFORMATION:
; APPLICANT: Klee, Harry J.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09437
; FILING DATE: 19911217
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,440
; FILING DATE: 26-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10538)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1377 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US91-09437-14

alignment_scores:
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  Ratio: 3.083       Gaps: 0
  Percent Similarity: 85.714      Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x PCT-US91-09437-14      ..

Align seg 1/1 to: PCT-US91-09437-14 from: 1 to: 1377

2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
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1314 GATTGATGGCTGCTTGGAGCTAAGATCGAACTCCGAC 1355

seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-476-008-2

seq_documentation_block:
; Sequence 2, Application US/08476008
; Patent No. 5627061
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306.063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749.611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576.537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1426
US-08-476-008-2

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:

US-09-485-529-104 x US-08-476-008-2 ..

Align seg 1/1 to: US-08-476-008-2 from: 1 to: 1982

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1373 GACCTGATGCCGGCTGGCGGGAAGATCGAATCTCCGAT 1414

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-306-063-2

seq_documentation_block:

; Sequence 2, Application US/083060603

; Patent No. 5633435

; GENERAL INFORMATION:

; APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306.063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749.611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576.537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1426
US-08-306-063-2

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:

US-09-485-529-104 x US-08-306-063-2 ..

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1373 GACCTGATGCCGGCTGGCGGGAAGATCGAATCTCCGAT 1414

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seq_documentation_block:

; Sequence 2, Application US/08833485

; Patent No. 5804425

; GENERAL INFORMATION:

; APPLICANT: Barry, Gerard F.

; APPLICANT: Kishore, Ganesh M.

; APPLICANT: Padgett, Stephen R.

APPLICANT: Stallings, William C.
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,485
FILING DATE: 07-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1426
US-08-833-485-2

alignment_scores:
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-137-440-2
seq_documentation_block:
; Sequence 2, Application US/09137440
; Patent No. 6248876
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.

APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgett, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 62..1426
US-09-137-440-2
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Quality: 37.00 Length: 14
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seq_documentation_block:
; Sequence 2, Application PCT/TUS9106148A
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.

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; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; TITLE OF INVENTION: Glyphosate Tolerant
; TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06148A
; FILING DATE: 19910828
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/749,611
; FILING DATE: 28-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10535)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1982 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; NAME/KEY: CDS
; LOCATION: 62..1426
;
PCT-US91-06148A-2

alignment_scores:
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  Ratio: 3.083       Gaps: 0
  Percent Similarity: 85.714   Percent Identity: 50.000

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seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-106-761-1

seq_documentation_block:
; Sequence 1, Application US/08106761
; Patent No. 5445956
; GENERAL INFORMATION:
; APPLICANT: HAMMOCK, Bruce D.
; APPLICANT: GRANT, David F.
; APPLICANT: BEETHAM, Jeffrey K.
; TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
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;
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
; STREET: Steuart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,761
; FILING DATE: 19930813
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 2307E-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2101 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 42..1703
;
US-08-106-761-1

alignment_scores:
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  Percent Similarity: 69.231   Percent Identity: 61.538

alignment_block:
US-09-485-529-104 x US-08-106-761-1 ..
Align seg 1/1 to: US-08-106-761-1 from: 1 to: 2101
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seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-09-629-616-1

seq_documentation_block:
; Sequence 1, Application US/09629616
; Patent No. 6255086
; GENERAL INFORMATION:
; APPLICANT: KUWABARA, Yoko
; APPLICANT: HASHIGUCHI, Kenichi
; APPLICANT: NAKAMATSU, Tsuyoshi
; APPLICANT: KURAHASHI, Osamu
; APPLICANT: MORI, Yukiko
; APPLICANT: ITO, Hisao
; TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM
; TITLE OF INVENTION: BACTERIA AND METHOD FOR PRODUCING L-ARGININE
; FILE REFERENCE: OP945CIP
; CURRENT APPLICATION NUMBER: US/09/629,616
; CURRENT FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
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; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-5

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 91.667 Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x US-09-629-616-1 ..
Align seg 1/1 to: US-09-629-616-1 from: 1 to: 4837

4 LeuAlaLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
|||||:|||||:|||||:|||||:|||||:
4452 CTGGCGTGGTGGCTCAAGATCTCTGCCACCGAA 4487

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-1

seq_documentation_block:
; Sequence 1, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-1

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x US-09-182-117-1 ..
Align seg 1/1 to: US-09-182-117-1 from: 1 to: 8012

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
|||||:|||||:|||||:|||||:|||||:
2258 GATTGTGATGGTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 2299

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-5

seq_documentation_block:
; Sequence 5, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8798 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-4

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x US-09-182-117-5 ..
Align seg 1/1 to: US-09-182-117-5 from: 1 to: 8418

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
|||||:|||||:|||||:|||||:|||||:
2237 GATTGTGATGGTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 2278

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-4

seq_documentation_block:
; Sequence 4, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8798 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-4

alignment_scores:
Quality: 37.00 Length: 14
Ratio: 3.083 Gaps: 0
Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x US-09-182-117-5 ..
Align seg 1/1 to: US-09-182-117-5 from: 1 to: 8418

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
|||||:|||||:|||||:|||||:|||||:
2237 GATTGTGATGGTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 2278

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-4

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Percent Similarity: 85.714 Percent Identity: 50.000

alignment_block:
US-09-485-529-104 x US-09-182-117-4 ..

Align seg 1/1 to: US-09-182-117-4 from: 1 to: 8798

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSerAsp 15
:::||||:||||| |||::: |||||
2347 GATTGATGGCTGCTTGGAGCTAAGATCAAGTCTCCGAC 2388

seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-472-217-1

seq_documentation_block:
; Sequence 1, Application US/08472217
; Patent No. 5726058
; GENERAL INFORMATION:
; APPLICANT: Alanen-Kurki, Leena
; APPLICANT: Auvinen, Petri
; APPLICANT: Jaakkola, Panu
; APPLICANT: Jalkanen, Markku
; APPLICANT: Lepp, Sirpa
; APPLICANT: Mali, Markku
; APPLICANT: Vihinen, Tapani
; APPLICANT: W rri, Anni
; TITLE OF INVENTION: Syndecan Stimulation Of Cellular
; TITLE OF INVENTION: Differentiation
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,217
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/206,186
; FILING DATE: 07-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,427
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0050003
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(4378..4443, 22026..22106, 23001..23483,
; LOCATION: 23905..24039, 24251..24418)
; US-08-472-217-1

alignment_scores:
Quality: 37.00 Length: 13
Ratio: 3.700 Gaps: 0
Percent Similarity: 76.923 Percent Identity: 61.538

alignment_block:
US-09-485-529-104 x US-08-472-217-1/rev ..

Align seg 1/1 to reverse of: US-08-472-217-1 from: 1 to: 26700

2 GluLeuLeuAlaLeuGlyTyrLysValArgAlaSer 14
||||||| ::| |||||::| ||||| |||
8341 GAATGCTAAGAGTTCAAGTCAAGTACCGAGTGAGTCACT 8303

seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-488-199-5

seq_documentation_block:
; Sequence 5, Application US/08488199
; Patent No. 5851993
; GENERAL INFORMATION:
; APPLICANT: Jalkanen, Markku
; APPLICANT: Mali, Markku
; TITLE OF INVENTION: Suppression of Tumor Cell Growth By
; TITLE OF INVENTION: Syndecan-1 Ectodomain
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,199
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,862
; FILING DATE: 13-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1102.0130001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4378..4443
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 22026..22107
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23002..23483
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 23905..24040
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 24252..24418
; US-08-488-199-5

alignment_scores:
Quality: 37.00 Length: 13
Ratio: 3.700 Gaps: 0
Percent Similarity: 76.923 Percent Identity: 61.538
alignment_block:
US-09-485-529-104 x US-08-488-199-5/rev ..
Align seg 1/1 to reverse of: US-08-488-199-5 from: 1 to: 26700
2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
||||||| : : ||||| : ||||| |||
8341 GAATTGCTAAGAGTTCAAGGCTACCGAGTGAGGATCAGT 8303

